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Minimum
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1: /cgn2_6/ptodata/2/pubpaa/USOS_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USOS_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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16.652 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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(c) 1993 - 2006 Biocceleration Ltd.
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US-11-150-054A-21
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US-11-165-211-52
US-11-165-211-52
US-11-165-226-62
US-11-214-199-10
US-11-214-199-12
US-11-021-689-742-70
US-11-078-469-32
US-11-078-469-33
US-11-078-469-33
US-11-078-469-62
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US-11-078-469-62
US-11-03-308-150
US-11-03-308-150
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52, Appl
62, Appl
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12, Appl
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70, Appl
33, Appl
33, Appl
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50.0	50.0	50.0	50.0	50.0	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	
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•	35, Appl	32, Appl	2549, Ap	63, Appl	1188, Ap	786, App	Appli	409, App	286, App	410, App	1120, Ap	36, Appl	5630, Ap	-	19, Appl		44, Appl		3030, Ap	

ALIGNMENTS

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Sequence 21, Application US/11150054A
Publication No. US20050278801A1
GENERAL INFORMATION:
APPLICANT: Lassner, Michael
APPLICANT: Wilkinson, Jack Q.
TITLE OF INVENTION: Plastid Transit Peptides
FILE REFERENCE: 2119-4284US1
CURRENT APPLICATION NUMBER: US/11/150,054A
CURRENT FILING DATE: 2005-06-09
PRIOR APPLICATION NUMBER: 60/578,535
PRIOR FILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.3
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-150-054A-13
Sequence 13 Application US/11150054A
Publication No. US20050278801A1
GENERAL INFORMATION:
APPLICANT: Lasener, Michael
APPLICANT: Wilkinson, Jack Q.
TITLE OF INVENTION: Plastid Transit Peptides
FILE REFERENCE: 2119-4284US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: synthetic peptide US-11-150-054A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/150,054A
CURRENT FILING DATE: 2005-06-09
PRIOR APPLICATION NUMBER: 60/578,535
PRIOR FILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PATENTIN VERBION 3.3
SEQ ID NO 13
LENGTH: 54
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Similarity 58.3%;
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CURRENT APPLICATION NUMBER: US/11/165,211
CURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: JP2004-189012
PRIOR FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 52
LENGTH: 327
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                Query Match
Best Local Similarity
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                                                                                           ; TYPE: PRT ; ORGANISM: Escherichia coli US-11-165-211-52
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                                                                                                                                                                                                                                                              Sequence 52, Application US/11165211
Publication No. US20050287626A1
GENERAL INFORMATION:
APPLICANT: KYOMA HAKKO KOGYO CO., LTD.
TITLE OF INVENTION: Process for producing dipeptides
FILE REFERENCE: 4093-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.3
SEQ ID NO 26
LENGTH: 54
TYPE: PRT
ORGANISM: artificial sequence
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Publication No. US20050278801A1
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CURRENT FILING DATE: 2005-06-09
PRIOR APPLICATION NUMBER: 60/578,535
PRIOR FILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lassner, Michael APPLICANT: Wilkinson, Jack Q.
TITLE OF INVENTION: Plastid Transit Peptides
FILE REFERENCE: 2119-4284US1
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ORGANISM: artificial sequence
FEATURE:
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OTHER INFORMATION: synthetic peptide
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5 KSTRRQR 11
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58.3%; Pred. No.
                                            58.6%; Score 34;
100.0%; Pred. No.
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Query Match
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US-11-165-226-62
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Publication No. US20050287627A1
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
TITLE OF INVENTION: Process for producing dipeptides or dipeptide derivatives
FILE REFERENCE: 4093-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/11/165,226
CURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: JP2004-189007
PRIOR FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HILTON,
APPLICANT: ALEXAND
APPLICANT: VINEY,
APPLICANT: WILLSON
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                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 10
                                                                       Matches
                                                                                      Best Local Similarity
                                                                                                       Query Match
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APPLICANT: NICHOLF, Donald
APPLICANT: NICOLF, Nicos A
APPLICANT: NICOLF, Nicos A
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC PROTEINS COMPRISING A SOCS
TITLE OF INVENTION: BOX
TITLE OF INVENTION UNMBER: US/11/214,199
CURRENT PEPLICATION NUMBER: US/09/908,805
PRIOR APPLICATION NUMBER: US/09/908,805
PRIOR PILLING DATE: 2001-07-19
PRIOR PILLING DATE: 2001-07-19
PRIOR PILLING DATE: 109/302,769
PRIOR FILLING DATE: 1999-04-30
                                                                                                                                                        LENGTH: 211
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-04-30 NUMBER OF SEQ ID NOS: 81
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159 RRMLGAPLRORR 170
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                                 1 RKMLKSTRRORR 12
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                                                                       Conservative
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                                                                   Pred. No. 35;
2; Mismatches
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Pred. No.
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; LENGTH: 212
; TYPE: PRT
; ORGANISM: Rat
US-11-214-199-12
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; LENGTH: 212
; TYPE: PRT
; ORGANISM: Mouse
US-11-214-199-4
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CURRENT FILING DATE: 2005-08-29
PRIOR APPLICATION NUMBER: US/09/908,805
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/302,769
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/112 Publication No. US20060003377A1 GENERAL INFORMATION:
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Publication No. US20060003377A1
GENERAL INFORMATION:
                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 12
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     Query Match
Best Local Similarity
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                                                                                                                                                              APPLICANT: NICHOLSON, Sandra E
APPLICANT: NICOLA, NICOS A
APPLICANT: NICOLA, NICOS A
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC PROTEINS COMPRISING A SOCS
TITLE OF INVENTION: SOX
FILE REFERENCE: 10976ZA
CURRENT APPLICATION NUMBER: US/11/214,199
CURRENT FILING DATE: 2005-08-29
PRIOR APPLICATION NUMBER: US/09/908,805
PRIOR APPLICATION NUMBER: US/09/908,805
PRIOR APPLICATION NUMBER: 09/302,769
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 81
NUMBER OF SEQ ID NOS: 81
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HILTON, Douglas J
APPLICANT: ALEXANDER, WATER
APPLICANT: VINEY, Elizabeth
APPLICANT: WILLSON, Tracey A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HILTON, Douglas J
APPLICANT: ALEXANDER, Warrer
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TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC PROTEINS COMPRISING A SOCS
TITLE OF INVENTION: BOX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 RRMLGAPLRORR 171
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VINEY, Elizabeth M
WILLSON, Tracev A
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VINEY, Elizabeth M
WILLSON, Tracey A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/11214199
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                                                                                                                                                                                                                                                                                                                                                                                                                         Robyn
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     55.2%;
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Pred. No. 35;
     Score
Pred.
DB
35;
                       7;
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                       Length 212;
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; Sequence 70, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
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US-11-092-168-8
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LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766.000091.10
CURRENT APPLICATION NUMBER: US/10/689,742
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: 09/746,783
PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-10-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PRÔTEIN KINASE INHIBITORS FILE REFERENCE: 920214.00003CONT3 CURRENT APPLICATION NUMBER: US/11/092,168 CURRENT FILING DATE: 2005-03-29
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PRIOR FILING DATE: 2004-10-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KMLKSTRR 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vankayalapati, Hariprasad
Bashyam, Sridevi
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Von Hoff, Daniel D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bearss, David J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Montigen Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Warner, Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Munoz, Ruben M.
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87.5%;
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Pred. No. 72;
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NUMBER OF SEQ ID NOS: 231 SOFTWARE: PatentIn version SEQ ID NO 70

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                                                                                                                    ; NAME/KEY: MOD_RES
; LCCATION: (1)
; OTHER INFORMATION: Ac-Thr
US-11-078-469-32
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Best Local S
Matches 6
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PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 32
LENGTH: 27
                                                Query Match 53.4%;
Best Local Similarity 41.7%;
Matches 5; Conservative
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Publication No. US20050282755A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: STOLOW, DAVID
APPLICANT: CONOER, DEE
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ANS-2001-UT
CURRENT APPLICATION NUMBER: US/11/078,469
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US/54,526
PRIOR FILING DATE: 2004-03-18
PRIOR FILING DATE: 2004-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HART, SCOTT A.
APPLICANT: ZEH, KARIN
APPLICANT: MACHLEIDT, THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (117)...(118)
OTHER INFORMATION: Xaa can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (107)...(107) OTHER INFORMATION: Xaa
                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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LOCATION: (645)..(645)
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                                                                                                                                                                                                                                           FEATURE:
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RKMLKSTRRORR 12
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                                                                                                                                                                                                        Description of Artificial Sequence: Synthetic peptide moiety
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                                                   4.
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Pred. No. 1.2e+02;
                                                                   Score 31; I
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      any naturally occurring
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                                                     Mismatches
                                                                                   DB 7;
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                                                                                     Length 27;
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                                                   Indels
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APPLICANT: STOLOW, DAVID
APPLICANT: CONGER, DEE
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ANS-2001-UT
CURRENT APPLICATION NUMBER: US/11/078,469
CURRENT FILING DATE: 2004-03-11
PRIOR APPLICATION NUMBER: 60/554,526
PRIOR APPLICATION NUMBER: 60/518,948
PRIOR FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: 60/618,948
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 3:
SEQ ID NO 3:
SEQ ID NO 3:
SEQ ID NO 3:
CHART SEPARATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide moiety
               FILE REFERENCE: ANS-2001-UT
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 00/554,526
PRIOR APPLICATION NUMBER: 60/554,526
PRIOR APPLICATION NUMBER: 60/618,948
PRIOR FILING DATE: 2004-10-15
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PATENTIN Ver. 3.3
SEQ ID NO 24
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Watches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-078-469-33; Sequence 33, App.; Publication No.
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APPLICANT: HART, SCOTT A.
APPLICANT: ZEH, KARIN
APPLICANT: MACHLEIDT, TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/11078469 Publication No. US20050282755A1
                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HART, SCOTT A.
APPLICANT: ZEH, KARIN
APPLICANT: MACHLEIDT, THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Ac-Thr
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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41.7%;
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OTHER INFORMATION: peptide moiety

NAME/KEY: MOD_RES

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Sequence 146, Application US/11120308
Publication No. US20060005277A1
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: MINION: CDNAS Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: US/11/120,308
CURRENT FILING DATE: 2005-05-02
PRIOR APPLICATION NUMBER: US/10/078,770
PRIOR FILING DATE: 2002-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/554,526
PRIOR FILING DATE: 2004-03-18
PRIOR FILING DATE: 2004-10-15
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 62
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
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; LOCATION: (1)
; OTHER INFORMATION: AC-Thr
US-11-078-469-62
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US-11-078-469-62
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US-11-120-308-146
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Best Local Similarity 41.7%;
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CONGER, DES
APPLICANT: CONGER, DES
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ANS-2001-UT
CURRENT APPLICATION NUMBER: US/11/078,469
CURRENT FILING DATE: 2005-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HART, SCOTT A.
APPLICANT: ZEH, KARIN
APPLICANT: MACHLEIDT, THOMAS
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide moiety
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Pred. No. 6.6;
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; LENGTH: 119
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-120-308-146
Search completed: February 4, 2006, 03:47:58
Job time: 9.44444 secs
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                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 196
SOFTWARE: Microsoft Office 97
SEQ ID NO 146
                                                                                                                                                                       Query Match 53.4%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILLING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,409
PRIOR FILLING DATE: 1999-07-12
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PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/157,401
PRIOR FILING DATE: 1999-10-01
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PRIOR FILING DATE: 2000-07-12
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 4, 2006, 03:26:33 ; Search time 248.444 Seconds (without alignments)
21.222 Million cell updates/sec
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cell transport.

02-DEC-2004 ADS17617;

(first entry)

ADS17617 standard; peptide; 12

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protein transduction domain; PTD; PTD-cargo moiety complex; cell immortalisation; cell viability; internalising peptide.

Amino acid sequence of protein transduction

domain (PTD) peptide

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ALIGNMENTS

RRESULT 1
ADS17617
ID ADS17617
AC ADS1
AC ADS1 04-MAR-2003; 2003US-0451243P. 03-MAR-2004; 2004US-00790768. Synthetic WPI; 2004-653708/63 04-MAR-2004; 2004WO-US006445 16-SEP-2004. WO2004078933-A2 (BIOW-) BIOWHITTAKER TECHNOLOGIES

New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell. to an

Claim 1; SEQ ID NO 1; 60pp; English.

The present sequence represents a peptide which functions as a protein transduction domain (PTD), and is capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. The present sequence is a reverse isomer of ADS17641, a previously identified internalising

Sequence 12 AA;

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RESULT 3
ADS17630
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Best Local Similarity 100.0%;
Matches 12; Conservative 0
                                                                                                                                                                                                                                                 Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                    The specification describes peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. The present sequence represents PTD peptide used in an experiment to determine the transduction efficiency of inverted isomers of PTDs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell.
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03-MAR-2004;
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                                                                                                                                                                                                                                                                                                                                   Sequence 15
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Modified-site
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2004US-00790768.
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tive 0;
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                                                                                                                                                                                                                          Score 58; DB 8;
Pred. No. 0.0078;
Mismatches 0
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Pred. No. 0.0063;
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                                                                                                                                                                                                                                                                             Length 15;
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Best Local Similarity
Matches 12; Conserv
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                                                   protein transduction domain; PTD; PTD-cargo moiety complex; cell immortalisation; cell viability; internalising peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids
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03-MAR-2004; 2004US-00790768.
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                                                                                                                                        Amino acid
                                                                                                                                                                                           02-DEC-2004
                                                                                                                                                                                                                                                ADS17618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO 14; 60pp; English.
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                                                                                                                                                                                                                                                                                                 ADS17618 standard; peptide; 15
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                                                                                                                                     sequence of protein transduction
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    cell viability; internalising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "biotin attached"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58; DB 8;
Pred. No. 0.0078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell.
                                                                                  04-MAR-2003; 2003US-0451243P.
03-MAR-2004; 2004US-00790768.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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03-MAR-2004; 2004US-00790768.
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                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                               (BIOW-) BIOWHITTAKER TECHNOLOGIES INC
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Pred. No.
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                                                                                                                                                                                                                                                      New isolated and purified polypeptide with a protein transduction domain, useful for delivering small molecules, proteins and nucleic acids to an
                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-653708/63.
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03-MAR-2004; 2004US-00790768.
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cell immortalisation; cell viability; internalising peptide;
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12; Conserv
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Pred. No.
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The present sequence represents a peptide which functions as a protein transduction domain (PTD), and is capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise

Disclosure; SEQ ID NO 4; 60pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells and increase cell viability in culture. The present PTD has lysine linker and a nuclear localisation signal.
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2004US-00790768.
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Pred. No.
                                                                                                    Score 58; DB 8; Length 21; Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell.
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03-MAR-2004; 2004US-00790768.
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cell immortalisation; cell viability; internalising peptide;
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                           protein transduction domain; PTD; PTD-cargo moiety complex;
cell immortalisation; cell viability; internalising peptide
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                                                                                                                                                                                                                                                                                                                                                      protein transduction domain; PTD; PTD-cargo moiety complex; cell immortalisation; cell viability; internalising peptide;
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  04-MAR-2004; 2004WO-US006445.
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03-MAR-2004; 2004US-00790768.
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100.0%; Pr
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RESULT 11
ADS17637
ID ADS177
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Best Local (
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                                                                                                                                                                                                                              04-MAR-2003; 2003US-0451243P.
03-MAR-2004; 2004US-00790768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein transduction domain; PTD; PTD-cargo moiety complex;
cell immortalisation; cell viability; internalising peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a PTD designated peptide 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-2004
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03-MAR-2004; 2004US-00790768.
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                                                                                                                                                                         (BIOW-) BIOWHITTAKER TECHNOLOGIES
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Pred. No.
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WPI; 2004-653708/63.

New isolated and purified polypeptide with a protein transduction domain,

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RESULT 12
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Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell.
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the treatment, prevention and diagnosis of medic.
P. acnes. The disorders include SAPHO syndrome (to pustulosis, hypertosis and osteomyelitis), uveit.
P. acnes is also involved in infections of bone,
                                                   polypeptides. The proteins and
                                                                  Sequences AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                            Example 1; SEQ ID NO 11720;
                                                                                                                                 Propionibacterium acnes vaccinating against and
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02-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes.
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ve J, Zhang
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2000US-0208841P.
2000US-0216747P.
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                                                                                                                    vulgaris.
                                        The proteins and their associated DNA sequences are use prevention and diagnosis of medical conditions caused
                                                                                                                                                                                                                                                       CORP
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                                                                                                                                 polypeptides and nucleic acids useful for diagnosing infections, especially useful
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                                                                                                                                                                                                               Mitcham JL, Wan
, Jen S, Carter
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                                                                                           1069pp; English.
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Pred. No.
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             rome (synovitis, acne, uveitis and endophthalmitis.
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RESULT 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitcham (Zhang Y, Barth B,
                           The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; antibodies against polypeptide of the invention; antibodies specific for a P. acnes method for stimulating an immune response specific for a P. acnes
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                                                                                                                                                                                                                                                                                                                                              New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
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                                                                                                                                                                                                                                                                                              Example
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DB; ACF64478.
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9; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang S, Jen S, Lou
Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                 SEQ ID NO 11720; 1481pp; English.
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ing S, Jen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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75.0%;
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Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Benson
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Benson DR,
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and an isolated T cell

comprising

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RESULT 14
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ID ADJ70
AC MAINTILE
AC ADJ70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huntington's disease; osteoarthritis; LHON; Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
                                comprises detecting a modified polypeptide with the disease.
                                                                                                Identifying a mitochondrial target for drug screening assays and treating diseases associated with altered mitochondrial function.
                                                                                                                                                                                                        WPI, 2003-845369/78
                                                                                                                                                                                                                                                                                                        Ghogh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteopathic; ophthalmological; cytostatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human heat mitochondrial protein as a therapeutic target SeqID2219.
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                                                                                                                                                                                                                                                                                                                                                                            (BUCK-)
                                                                                                                                                                                                                                                      n SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                                                                                                                                                                                         BUCK INS
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                                                                                                                                                                                                                                                                                                        Gibson BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assay; diabetes mellitus;
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                                                                                                                                                                                                                                                                                                        Taylor SW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                  Nakagawa
Tateishi
                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                 WPI; 2001-376931/40.
N-PSDB; AAH65429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1999; 99JP-00377484
07-APR-2000; 2000JP-00159162
03-AUG-2000; 2000JP-00280988
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                                                                                                                                                                Claim 17; SEQ ID NO 3964; 246pp + Sequence Listing; English
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Senoh A, Ikeda
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da M,
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Ozaki A;
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suc present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from

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Perfect score:
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ALIGNMENTS

RESULT

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C;Species: Mycobacterium leprae
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87213
R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler,
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.;
eam, M.A.; Rutherford, K.M.
Mature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002 hypothetical protein SCE68.25c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Apte: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36275
C;Accession: T36275
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21576
A;Accession: T36275
A;Accession: T36275
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-32 cMUR>
A;Cross-references: UNIPROT: Q9WX07; UNIPARC: UPI0000DB13D; EMBL;AL079345; PIDN: CAB45361.
A;Genetics:
C;Genetics:
A;Genetics: SCOEDB: SCE68.25c Query Match
Best Local Similarity
Best Accal Similarity
Conserve A;Cross-references: UNIPROT:Q9CB56; UNIPARC:UPI0000139A1B; GB:AL450380; NID:g13094003; PC;Genetics: A;Gene: ML2428A 멼 δ A; Molecule type: DNA A; Residues: 1-33 <ST A; Status: preliminary Matches Query Match N Local 18 1 RKMLKSTRRQRR Similarity 9; Conserv RKLLKRTRVORR <STO> Conservative Conservative 67.2%; 72.4%; 12 29 Score 42; DB 2; Pred. No. 0.63; 1; Mismatches Score 39; I Pred. No. 2 Mismatches DB 2.2; DB 2; 2 ب. در 2 Length 33; Length 32; Indels Indels Skelton, J.; Squares, R.; <u>..</u> 0 Gaps Gaps 0 0 P.R.; Ho Holroyd,

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RESULT 4
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A;Cross-references: UNIROT:08YX34; UNIPARC:UPI00000CE09F; GB:BA000019; PIDN:BAB73341.1
A:Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABC transporter ATP-binding protein alr1384 [imported] - Nostoc sp. (strain PCC C;Species: Nostoc sp. PCC 7120 C;Species: Nostoc sp. strain PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 31-Dec-2004 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 31-Dec-2004 C;Accession: AE1979
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A;Accession: T24499
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; submitted to the Protein Sequence Database, June A;Reference number: Z16897
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A; Introns: 25/3; 134/2; 157/1; 211/2
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A;Experimental source: clone T05A6
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A; Residues: 1-258 <WIL>
                                                         protein kinase homolog T30C3.60 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) (;Cpecies: Arabidopsis thaliana (mouse-ear cress) (;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T10219
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protamine P1 - 1
C;Species: Tachy
C;Date: 07-Oct-1
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C; Superfamily: 8;
C; Keywords: DNA
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S39424
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A;Residues: 1-651 <BEV>
A;Residues: 1-651 <BEV>
A;Cross-references: UNIPROT:Q9STJ8; UNIPARC:UPI00000489E8; EMBL:AL079350; GSPDB:GN00062;
A;Cross-references: cultivar Columbia; BAC clone T30C3
C;Genetics:
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T29995
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A;Map position: 4
                                                                                                                                                                                                                                                                                                                       hypothetical protein C43H6.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #tcC;Accession: T29995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 218, 457-461, 1993
A; Title: Evolution of the monotremes. The sequences of the A; Reference number: S39424; MUID:94094837; PMID:8269934
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                                                                                                                                                                           A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-89 <LET>
                                                                                                                                                                                                                                 A, Description: The sequence A, Reference number: Z20717 A, Accession: T29995
                                                                      A; Map position:
A; Introns: 42/2
                                                                                                          A; Gene: CESP: C43H6.8
                                                                                                                                         A;Cross-references: UNIPROT:Q18590; UNIPARC:UPI0000077B96; EMBL:U51999; PIDN:AAA96089.1;
A;Experimental source: strain Bristol N2; clone C43H6
                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, March A;Description: The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT: P35311; UNIPARC: UPI000016C71A; EMBL: Z26848; NID: g407183;
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A;Residues: 1-69 <RET>
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;Species: Tachyglossus aculeatus (Australian echidna)
;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
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;Keywords: DNA binding
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 Score 36; DB
Pred. No. 18;
3; Mismatches
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RKMLKSTRRQRR 12

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A.; ROBE, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997

8;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H65035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RiPerna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
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C;Species: phage Pf1
C;Species: phage Pf1
C;Date: 18-Feb-1994 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Date: 18-Feb-1994 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Acccesion: S15.53; S20824
R;Hill, D.F.; Short, N.J.; Perham, R.N.; Petersen, G.B.
J. Mol. Biol. 218, 349-364, 1991
                                                                                                                                             C;Accession: H65035
R;Blattner, F.R.; Plunkett III,
                                                                                                                                                                                              hypothetical protein srmB-ung intergenic region - Escherichia coli (strain C;Species: Escherichia coli (C;Species: Escherichia coli (C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
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C;Superfamily: HTH-type transcriptional regulator,
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A;Cross-references: UNIPROT:Q8X5A8; UNIPARC:UPI00000D0CE5; GB:AE005174; NID:g12516998;
A;Experimental source: strain O157:H7, substrain EDL933
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                    A;Status: preliminary; nucleic acid sequence
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C<sub>I</sub>Species: Escherichia coli
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A;Cross-references: UNIPROT:P25132; UNIPARC:UPI00001384CE; EMBL:X52107; NID:g14829; PIDN
A;Experimental source: ATCC 25102-B1
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                                                                                                                                    G.; Bloch, C.A.; Perna, Y.
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Pred. No. 86;
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K.; Apodaca,
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A;Cross-references: UNIPARC:UPI000006BD1D;
C;Superfamily: RNA-directed RNA polymerase
C;Keywords: nucleotidvltransferase
                                                                                                                      A;Cross-references: UNIPROT:P25328; UNIPARC:UPI0000134B87; (R;Matsumoto, Y.; Wickner, R.B.
J. Biol. Chem. 266, 12779-12783, 1991
A;Title: Yeast 20 S RNA replicon. Replication intermediates A;Reference number: A40895; MUID:91286318; PMID:1648104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C91059
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C,Species: Becherichia coli
C,Date: 18-Jul-2001 #~~~~
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A;Gene: EC63443
C;Superfamily: HTH-type transcriptional regulator,
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C;Superfamily: HTH-type transcriptional regulator,
                                                                                                                                                                                                                                                                                        R;Rodriguez-Cousino, N.; Esteban, L.M.; Esteban, R. J. Biol. Chem. 266, 12772-12778, 1991
A;Title: Molecular cloning and characterization of W double-stranded A;Reference number: A40894; MUID:91286317; PMID:2061340
                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Saccharomyces cerevisiae
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-308 <HAY>
                                                                            A; Molecule type: genomic RNA
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A; Residues: 1-829 < ROD>
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A;Experimental source: strain K-12, substrain MG1655
                                                               A;Residues: 1-825,'V' <MAT>
                                                                                                      A;Accession: A40895
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Best Local
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Pred. No. 86;
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                   GB:M64034; NID:g335015; in W dsRNA
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86;
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50.0%;

Score Pred.

No.

DB 2; 2.1e+02;

Length

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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID: 21016719; PMID: 11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Engeland, B.; Neu, A.; Ludwig, J.; Roeper, J.; Pongs, submitted to the EMBL Data Library, July 1998 A;Description: Identification of three rat potassium characteristics.
                      RESULT 15
T09127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F15K9.2 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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probable erythrocyte-binding protein MAEBL - Plasmodium yoelii
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                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                     A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-1020 <STO>
A,Residues: 1-1020 <STO>
A,Cross-references: UNIPROT:Q9ZVT9; UNIPARC:UPI000017CB88; GB:AE005172; NID:g3850588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
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A;Residues: 1-1017 <ENG>
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                                                                                                                                                                                                                                                                               A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Gene: elkl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: E86165
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                                                                                                           978
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                                                                                                                                                 4 LKSTRRORR 12
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Similarity 77.8%;
7; Conservation
                                                                                                                                                                                          Similarity 77.177; Conservative
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                                                                                                         LKSTRHQKR 986
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                                                                                                                                                                                                                  Score 35;
Pred. No.
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C;Accession: T09127 R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H. Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998 A;Title: A family of chimeric erythrocyte binding proteins of malaria parasites. A;Reference number: Z16577; MUID:98115903; PMID:9448314 A;Accession: T09127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Plasmodium yoelii
C;Date: 11-Jun-1999 #sequence
C;Accession: T09127
                                                                                                                                                                                                                                                                                                    A;Introns: 62/1; 1648/1; 1674/2; 1697/1
C;Keywords: alternative splicing; cell binding; erythrocyte invasion
                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1701 <KAP>
A;Residues: 1-1701 <KAP>
A;Cross-references: UNIPROT:O61164; UNIPARC:UPI000007D433; EMBL:AF031886; NID:g2947227;
A;Experimental source: subspecies yoelii; strain YM
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                                                                                                                                                                                                                                                                                                                                                      A;Gene: maebl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
Search completed: February
Job time : 24.6667 secs
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                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                     60.3%;
Local Similarity 58.3%;
les 7; Conservation
                                                                                                    1354 KKRLKRORKORR 1365
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                       4
                          2006,
                                                                                                                                                                                                     2; Mismatches
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Pred. No. 4.1e+02;
                            03:42:20
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                                                                                                                                                                                                        Indels
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated

- permanent accession numbers. The new UniProt record may not contain the previous temporary accession number. numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession
- accession number can be found by searching the old accession number in the UniProt Protein extension .rup) that can no longer be found in the database, the permanent record with the new Archive database (UniPARC) at If you encounter an accession number from an older search run against UniProt (

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher

numbers. members of the public who may encounter UniProt temporary accession include a copy of this attachment to assist any future Examiners or When submitting sequence search results for scanning into IFW, please

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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(c) 1993 - 2006 Biocceleration
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  Y500A MYCTU
RS21 TREDE
C6NUK5 CORDI
O22196 CAEEL
O9UGR5 CAEEL
O9UGR5 CAEEL
O9UGR5 CAEEL
O9UGR5 CAEEL
O9UTY5 ORYSA
Q4WQN2 ASPFU
Q5VR29 ORYSA
Q7SH27 BRARE
Q7XH27 BRARE
Q7XH27 BRARE
Q8XX14 ANASP
Q522X1 MAGGR
Q7XH27 BRARE
Q8XX14 TETMG
Q522X1 TETMG
Q8LMH0 ORYSA
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Q6AAZ0 PROAC
Q6AAZ0 PROAC
Q9MX07 STRCO
Q4JSX2 CORJK
Q8FSGO CORED
Q8FMB6 ECOL6
Q8FMB6 ECOL6
Q9FMB6 ECOL6
Q9FMB6 MANSM
Y2428 MYCLE
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Q4ndy7 arthrobacte
Q4ndy7 arthrobacte
Q6aaz0 propionibac
Q9wx07 streptomyce
Q4jsx2 corynebacte
Q8feg0 corynebacte
Q8feg0 corynebacte
Q8febb6 escherichia
Q9ztl1 cyanidium c
Q65ub3 mannheinia
P0a5d0 mycobacteri
p0a5c9 mycobacteri
p0a5c9 mycobacteri
Q73j11 treponema d
Q6njk5 corynebacte
Q22198 caenorhabdi
Q9ubcr5 caenorhabdi
Q9ubcr5 caenorhabdi
Q9ubr5 caenorhabdi
Q9ubr5 caenorhabdi
Q9uvg1 aspergillus
Q5wm2 oryza sativ
Q4wq12 aspergillus
Q5wm2 oryza sativ
Q7xbc7 brachydanio
Q8yx34 anabaena sp
Q522y1 magnaporthe
Q4sja7 tetraodon n
Q8lmh0 oryza sativ
Q8s612 oryza sativ
Q8s612 oryza sativ
Q8y4x4 homo sapien
Q35738 mus musculu
Q8ww13 homo sapien
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AZO_PROAC
QGAAZO_PROAC PRELIMINARY;
QGAAZO;
QSAAZO;
25-OCT-2004 (TrEMBLrel. 28, L:
25-OCT-2004 (TrEMBLrel. 28, L:
25-OCT-2004 (TrEMBLrel. 28, L:
25-OCT-2004 (TrEMBLrel. 28, L:
45-OCT-2004 (TrEMBLrel. 28, L:
25-OCT-2004 (TrEMBLrel. 
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US DOE Joint Genome Institute (PGF-ORNL);

Larimer F., Land M.;

"Annotation of the draft genome assembly of Arthrobacter sp.

submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.

EMBL; AAHGG1000010; EAL95472.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 32 AA; 4083 MW; 3DFEAD9F6371E689 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., G
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Arthrobacter
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arthrobacter sp. FB24.
Bacteria; Actinobacteria; Actinomicrococcineae; Micrococcaceae;
          Propionibacterium acnes
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18 RKLLRKTRHQRR 29
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Q51R74_MAGGR
Q51R74_RAENI
Q9STUB_ARATH
Q4QAJ7_LEIMA
Q4QAJ7_LEIMA
Q4QAJ7_LAEPI
Q4GAJ7_CAE
Q62N3_CAEEL
Q62N3_CAEEL
Q8H2R3_CRYSA
Q61N3_BACAN
Q61N3_BACAN
Q652U2_CRYSA
P76887_ECOLI
Q9CW37_MOUSE
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Pred. No. 0.94;
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US-10-790-768A-1 58

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ID 04JSX2 CORJK PRELIMINARY;
AC Q4JSX2;
DT 13-SEP-2005 (TrEMBLrel. 3)
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STRAIN=A3(2) / M145;

MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;

MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.

Rabbinowitsch E., Rajandream M.A., Mutherford K.M., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.

Seeger K., Saunders D., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
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STRAIN-KPA171202 / DSM 16379;

PubMed=15286773; DOI=10.1126/science.1100330;

Brueggemann H., Henne A., Hoster F., Liesegan

Strittmatter A., Hujer S., Duerre P., Gottesch
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SEQUENCE
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SCO3327.
OrderedLocusNames=SCO3327; ORFNames=SCE68.25c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the coelicolor A3(2)."

Nature 417:141-147(2002).

EMBL; AL939116; CAB45361.1; -;

PIR; T36275; T36275.
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Complete proteome; Hypothetical protein.
SEQUENCE 33 AA; 4073 MW; 4256B042E26371E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Propionibacterineae; Propionibacteriaceae; Propionibacterium.
NCBI TaxID=1747;
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Science 305:671-673(2004).
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Pred. No. 0.97;
l; Mismatches
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, Gottschalk G.
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GO COREF
Q8FSGO COREF 1
Q8FSGO;
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Submitted (DEC-2004) to the
EMBL; CR931997; CAIJ8085.1;
Hypothetical protein.
SEQUENCE 33 AA; 4163 MW;
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Tauch A., Kaiser O., Hain T., Goesmann A., Welsshaar B
Albersmeier A., Bekel T., Bischoff N., Brune I., Chakr
Kalinowski J., Meyer F., Rupp O., Schneiker S., Viehoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium jeikelum (strain K411).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=306537;
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OrderedLocusNames=CE0433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete Genome Sequence and Analysis Nosocomial Pathogen Corynebacterium je Bacterium of the Human Skin Flora.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005
13-SEP-2005
                                                                             Genome Res. 13:1572-1579(2003).
EMBL; BA000035; BAC17243.1; -; (
Complete proteome; Hypothetical
SEQUENCE 33 AA; 4163 MW; 81
                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                       Corynebacterium efficiens
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Puhler A.;
                                                                                                                            replacements efficiens.";
                                                                                                                                                                  Gojobori T.;
                                                                                                                                                                                                                                                NCBI_TaxID=152794;
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                                                                                                                                                   "Comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol. 187:4671-4682(2005)
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RKMLKSTRRQRR
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4163 MW; 815
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ical protein.
8156A587F163D4F5
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Pred. No. 1.
                                                                                                                                        sequence analysis of the amino acid the thermostability of Corynebacter
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                                           Score 42; DB Pred. No. 1.5;
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QBNT95; Q6M7V
01-OCT-2002 (
01-OCT-2002 (
NUCLEOTIDE SEQUENCE.

STRAIN=06:H1 / CFT073 / ATCC 700928 / UPEC;

MEDLINE=22388234, PubMede12471157; DOI=10.1073/pnas.252529799;

Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stra

Rasko D., Buckles E.L., Zhou S., Schwartz D.C., Perna N.T.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sec

of uropathogenic Escherichia coil.";

proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative acid shock protein.
OrderedLocusNames=c1989;
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01-OCT-2002 (TEMBLrel. 22, Last sequence update)
13-SEP-2005 (TEMBLrel. 31, Last annotation update)
13-SEP-2005 (TEMBLrel. 31, Last annotation update)
Hypothetical protein Cg10413.
OrderedLocusNames=Cg10413, Cg9494;
Corynobacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBFHB6_ECOL6
QBFHB6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
MEDLINB=22830012; PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Kalinowski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
McHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,
McHardy A.C., Meyer F., Moeckel B., Ffefferle W., Puehler A.,
McHardy A.C., Rupch C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli 06.
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STRAIN=ATCC 13032 /
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Biotechnol. 104:5-25(2003).
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BX927149; CAF19130.1; -; Genomic DNA.
ete protecome; Hypothetical protein.
NCE 33 AA; 4163 MW; 8156A587F163D4F5
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Pred. No. 1.5;
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RESULT 9

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DE Unp protein.

GN Name=unp Orde

OS Mannheimia suc

OC Pasteurellacea

OX NCBI_TaxID=221
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R GO; GO:0003700; F:transcription factor activity; IEA.

R GO; GO:0006355; P:transcription infinition; IEA.

R GO; GO:0006352; P:transcription infinition; IEA.

R InterPro; IPR009042; Sigma70 r1 2.

R InterPro; IPR007624; Sigma70 r2.

R InterPro; IPR007624; Sigma70 r2.

R InterPro; IPR007630; Sigma70 r4.

R InterPro; IPR007630; Sigma70 r4.

R InterPro; IPR00943; Sigma70 r4.

R Pfam; PP00140; Sigma70 r1 2; 1.

R Pfam; PP04542; Sigma70 r2; 1.

R Pfam; PP04543; Sigma70 r4; 1.

R Pfam; PP04545; Sigma70 r4; 1.

R PFAMTS; PR00046; SIGMA70 r4; 1.

R PRINTS; PR00046; SIGMA70 r4; 1.

R PRINTS; PR00046; SIGMA70 r4; 1.
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                                                                     Uup protein.
Name=uup; OrderedLocusNames=MS0840;
Mannheimia succiniciproducens (strain MBEL55E).
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Complete proteome.
SEQUENCE 125 AA; 14911 MW;
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Mannheimia.
NCBI_TaxID=221988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Troxler R.F., Tan S., Liu B.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ
EMBL; AF050634; AAD02575.1; -; Genomic_DNA.
HSSP; Q9WX/B; 11W7.
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Cyanidium caldarium.
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01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=III-D-2;
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PROSITE; PS00716; SIGMA70_2; 1.
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006; Cole S.T., Biglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E., Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamilin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
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InterPro; IPR003499; ABC_transp_like.
Pfam; PF00005; ABC_transp_1.
ProDom; PD00006; ABC transporter; 1.
SMART; SM00382; AAA; 7.
SMART; SM00381; ABC_TRANSPORTER 1; UNKNOWN_2.
PROSITE; PS00813; ABC_TRANSPORTER_2; 2.
PROSITE; PS06893; ABC_TRANSPORTER_2; 2.
SEQUENCE 646 AA; 73203 MW; 1C31B0A365CE6BB6 CRC64;
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PubMed=15378067; DOI=10.1038/nbt1010;
Hong S.H., Kim J.S., Lee S.Y., In Y.H.,
Kim C.H., Jeong H., Hur C.G., Kim J.J.;
"The genome sequence of the capnophilic succiniciproducens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y2428 MYCLE STANDARD; PRT; P0A5DÖ, Q9CB56; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence up 10-MAY-2005 (Rel. 47, Last annotation Hypothetical protein ML4428.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                        EMBL; AL583925; CAC31945.
PIR; A87213; A87213.
                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                 "Massive gene decay in the Nature 409:1007-1011(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                    Leproma; ML2428A;
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SIMILARITY: Belongs to the ABC transporter
L; AED16827; AAU37447.1; -; Genomic_DNA.
GO:0005524; F:ATP binding; IEA.
GO:0016887; F:ATPase activity; IEA.
GO:0001666; F:nucleotide binding; IEA.
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ilarity 72.7%;
Conservative
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Hypothetical 4145 MW; 815
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98295987; PubMed=9634230; DOI=10.1038/31159; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin I Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R. Sulston J.E., Taylor K., Whitchead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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POA5C5; Q9CB56;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Hypothetical protein Rv0500.1/MT0521.1.
OrderedLocusNames=Rv0500.1, MT0521.1; ORFNames=Rv0500B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
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                          EMBL; BX842573; CAE55291.1; -;
EMBL; AE006953; -; NOT_ANNOTATE
TIGR; MT0521.1; -
Tuberculist; Rv0500B; -.
Complete proteome; Hypothetical
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STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
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                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22255591; PubMed=12368430; Camus J.-C., Pryor M.J., Medigue C., "Re-annotation of the genome sequence
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                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                       Microbiology 148:2967-2973(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION.
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                                                                                                                                                                                                                                                        veen the Swiss Institute of Bioinfo
European Bioinformatics Institute.
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                                                                                                                                                                                                                           long as its content is in no way modified and this statement
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                                                                                                                                                                                                                                                                                                                                                                                                                                  genome sequence of Mycobacterium tuberculosis
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Pred. No. 5.6;
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proteome;
33 AA;

Hypothetical 4145 MW; 819

al protein. 8156A587F16291F5 CRC64;

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RESULT 12
RESULT TREDE
ID RS21 TREDE
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RA DOGBOR RJ ,
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RA GEBREGUT J.,
RA WEINSTORM S.A.,
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     RESULT 13
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Best Local S
Matches 8
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InterPro; IPR001911, Ribosomal S21.
Pfam; PP01165, Ribosomal S21; 1.
PRINTS; PR00976; RIBOSOMALS21.
ProDom; PD005521; Ribosomal S21; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.
Dodson R.J., Davidsen T.M., DeBoy R.T., Fours D.E., Haft D.H.,
Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
Vashisth P., McNeill T.Z., Xiang Q., Sodergren B., Baca B.,
Wainstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.,
"Comparison of the genome of the oral pathogen Treponema denticola
with other spirochete genomes.",
Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE017254; AAS12990.1; -; Genomic_DNA.
TIGR; TDE2473; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
STRAIN=ATCC 35405 / DSM 14222;
PubMed=15064399; DOI=10.1073/pnas.0307639101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30S ribosomal protein S21.
Name=rpsU; OrderedLocusNames=TDE2473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the ribosomal protein S21P family.
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les 8; Conserv
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proteome; Ribonucleoprotein; Ribosomal protein.
69 AA; 8502 MW; 0D0698EE6C4B055C CRC64;
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     (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local S
Matches 8
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"Genome sequence of the nematode C. elegans
investigating biology.";
Science 282:2012-2018 (1998).
EMBL; Z50796; CAA90670.1; -; Genomic_DNA.
PIR; T24499; T24499.
Ensembl; T05A6.2; Caenorhabditis elegans.
WormBase; WBGene00000517; cki-2.
WormPap; T05A6.2a; CE1928.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004661; F:cyclin-dependent protein
GO; GO:0007050; P:cell cycle arrest; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation updat
Hypothetical protein cki-2.
Name=cki-2; ORFNames=T05A6.2, T05A6.2a;
                                                                                                                                                             InterPro; IPR003175; CDI.
Pfam; PP02234; CDI; 1.
Complete proteome; Hypothetical
SEQUENCE 258 AA; 28523 MW; 0
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MEDLINE=99069613; PubMed=9851916;
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STRAIN-BIOCTYPE GRAVIS / NCTC 13129;
MEDLINE=22565443; PubMed=14602910; DOI=10.1093/nar/gkg874;
MEDLINE=7-7-3 h -M Efstratiou A., Dover L.G., Holden M
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OrderedLocusNames=DIP0396;
Corynebacterium diphtheriae.
Bacteria; Actinobacteridae; Actinomycetales;
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NCBI_TaxID=6239;
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EMBL; BX248355; CAE48900.1; -; Genomic_DNA.
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                                                             Conservative
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                                                          Score 39; DB Pred. No. 50; Nismatches
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Pred. No. 13;
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06A1AF2400BDE4D6 CRC64;
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Search completed: February 4, 2006, 03:41:25
Job time : 139.556 Becs
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RX MEDLINE-99069613; PubMed-9851916;

RT The C. elegans sequencing consortium;

The C. elegans sequencing consortium;

RT investigating biology.";

RT investigating biology.";

RI Science 282:2012-2018(1998).

EMBL; APT79359; AAF12869.1; -; GROMIC_DNA.

DR EMBL; Z50796; CAD45597.1; -; GROMIC_DNA.

DR WormBase; WBGene00000517; cki-2.

DR WormBase; WBGene00000517; cki-2.

DR WormBase; WBGene00000517; cki-2.

DR GO; GO:0004631; F:kinase activity; IEA.

DR GO; GO:0004631; F:kinase activity; IEA.

DR GO; GO:0016301; 
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Best Local S
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Q9UGR5;
Q0UGR5,
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 31, Last annotation update)
Cyclin-dependent kinase inhibitor (Hypothetical protein cki-2).
Name=cki-2; QRFNames=T05A6.2, T05A6.2B;
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
Rhabditidae; Peloderinae; Caenorhabditis.
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STRAIN-N2 Bristol;
MEDLINE=20056449; PubMed=10587644; DOI=10.1038/70272;
MEDLINE=20056449; PubMed=10587644; DOI=10.1038/70272;
MEDLINE=20056449; PubMed=10587644; DOI=10.1038/70272;
MEDLINE=20056449; PubMed=10587644; DOI=10.1038/70272;
MEDLINE=2006449; PubMed=10587644; DOI=10.1038/70272;
MEDLINE=2006444; DOI=10.1038/70272;
MEDLINE=2006444; DOI=10.1038/70272;
MEDLINE=2006444; DOI=10.1038/70272;
MEDLINE=2006449; PubMed=10587644; DOI=10.1038/70272;
MEDLINE=2006444; DOI=10.1038/70272;
MEDLINE=2006444;
MEDLINE=2
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8; Conservative
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28156, 27153, 32723, 47940, 47947, 32196, 47413, 47413, 25470, 315248, 105248,

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Post-processing: Minimum Match
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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32.351 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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                        US-09-605-703B-2766
US-09-513-990C-8105
US-09-525-991A-27639
US-09-286-796A-25921
US-08-630-822A-60
US-09-005-609-60
US-09-171-156A-18
US-09-171-156A-18
US-09-134-000C-3832
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US-09-134-000C-3832
US-09-252-991A-22842
US-09-252-991A-22842
US-09-270-767-60600
US-09-270-767-59291
US-09-270-767-45108
US-09-270-767-43108
US-09-252-991A-20018
US-09-252-991A-10010
US-09-252-991A-10010
US-09-270-767-4388
US-09-270-767-4388
US-09-270-767-4388
US-09-270-767-4388
          5-09-270-767-43888

5-09-800-729-124

IS-10-104-047-2221

IS-09-081-385-151

IS-09-752-639-151
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59291, A
20018, A
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23448, A
18133, A
18133, A
18133, A
13888, A
2221, App
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60, Appl
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18, Appl
18, Appl
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3832, Ap
22842, A
23752, A
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8105, Ap
27639, A
25958, A
25921, A
Sequence 8155, Application US/09513999C
; Sequence 8155, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
   APPLICANT: Dumas Milne Edwards, J.B.
   APPLICANT: Duclert, A.
   APPLICANT: Duclert, A.
   APPLICANT: Giordano, J.Y.
   TITLE OF INVENTION: Expressed Sequence Tags and Enc.
   Patent No. 6783961
; PILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
ITILE OF INVENTION: PROTEINS
FILE REFERENCE: BGI-129CP
CURRENT APPLICATION UNMBER: US/09/605,703B
CURRENT APPLICATION NUMBER: 60/1-27,764
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
                                                                                                                                                                                  RESULT 2
US-09-513-999C-8105
                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 33
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-2766
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Matches 9
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SEQ ID NO 2766
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                                                                                                                                                                                                                                                                                                               Similarity
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US-09-800-729-89
US-09-288-796A-28156
US-09-287-991A-27153
US-09-270-767-32723
US-09-270-767-32196
US-09-270-767-32196
US-09-270-767-47943
US-09-270-767-47943
US-09-270-767-47943
US-09-270-767-47943
US-09-252-991A-31248
US-09-252-991A-17523
US-09-252-991A-17523
US-09-252-991A-17523
US-09-252-991A-17523
US-09-252-991A-17523
US-09-270-767-46596
US-09-999-002-517
US-10-360-101-259
US-09-999-002-519
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Pred. No.
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Length 33; Indels

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Gaps

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Encoded Human Proteins.

Regult No.

Minimum DB Maximum DB

Sequence:

Title:

Run on:

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APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27639
LENGTH: 107
             RESULT 4
US-09-252-991A-25958
; Sequence 25958, Application US/09252991A
; Patent No. 6551795
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US-09-252-991A-27639
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GENERAL INFORMATION:
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SEQ ID NO 8105
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Matches 7; Conser
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NAME/KEY: UNSURE
LOCATION: 24
OTHER INFORMATION: X
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OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
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OTHER INFORMATION:
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Similarity 66.7%;
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Pred. No. 23;
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 25921
LENGTH: 87
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US-09-248-796A-25921
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US-09-252-991A-25958
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN'
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
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SEQ ID NO 25958
LENGTH: 537
TYPE: PRT
                                                                                                                                                                                                                                    Sequence 60, Application US/08630822A Patent No. 5840695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Candida albicans
                                                                                 APPLICANT: FRANK, GLENN R.
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 6; Conserv
                        STREET:
                                            ADDRESSEE:
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Denver
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                      1700 Lincoln Street, Suite 3500
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                                              Sheridan Ross P.C.
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Pred. No. 71;
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Pred. No. 2.5e+02;
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COUNTRY: U.S.A

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CURRENT APPLICATION DATA,
APPLICATION NUMBER: U5/08/630,822A
FILLING DATE: 11-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-9700
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US-09-005-069-60
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PAPELICATION NUMBER: US/09/005,069
FILING DATE
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 08/630,822
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C3
TELECOMMUNICATION INFORMATION:
TELEPAN: (303) 863-0723
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 60, Applia
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Best Local Similarity 70.0%;
Matches 7; Conservative
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
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TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1700 Lincoln Street, Suite 3500
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                                                                                                                     2618-17-C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-005-069-60
RESULT 9
US-09-04-730A-18
; Sequence 18, Application US/09004730A
; Patent No. 6485968
; GENERAL INFORMATION:
                                                                                                                                                                                                      Query Match
Best Local Similarity
Thes 7; Conserve
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Best Local Similarity
Marches 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,156A
FILING DATE: 04-Mar-1999
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: COnnell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAN: 303/863-9700
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                                                                                                                                                                                                                                                                                                                      LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 80202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS P.C.
STREET: 1560 BROADWAY, SUITE 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA APPARATUS TO COLLECT SUCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hunter, Shirley Wu
Sim, Gek-Kee
                                                                                                                                           100 ŘKVĽESVŘŘÓ 109
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Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
2; Mismatches 1
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; SEQ ID NO 18; LENGTH: 157; TYPE: PRT; ORGANISM: Ctenocephalides felis US-09-004-730A-18
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                                                                                                                                                                       RESULT 11
US-09-134-000C-3832
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GENERAL INFORMATION:
APPLICANT: LYNN DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPE
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 2618-17-C5-PUS-1
CURRENT APPLICATION NUMBER: US/09/004,730A
CURRENT FILING DATE: 1998-01-08
PRIOR FILING DATE: 1997-10-16
NUMBER OF ENG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/08981799A Patent No. 6576238
                                                                                                                               Sequence 3832, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity 70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Weber, Eric
APPLICANT: Wu Hunter, Shirley
APPLICANT: Sim, Gek-Kee
APPLICANT: Frank, Glenn
APPLICANT: Frank, Glenn
APPLICANT: Wallenfels, Lynda
APPLICANT: Wallenfels, Lynda
APPLICANT: Wallenfels, Lynda
APPLICANT: Wovel ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SU
TITLE OF INVENTION: PROTEINS"
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APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/08/981,799A
CURRENT FILING DATE: 1998-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/97/18669
PRIOR FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 157
TYPE: PRT
ORGANISM: Ctenocephalides felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                 100 RKVLESVRRQ 109
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Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
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                                                              AND THERAPEUTICS
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Sequence 22842, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO F

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

PILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                  FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT ; ORGANISM: Enterococcus faecalis US-09-134-000C-3832
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US-09-252-991A-22842
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US-09-252-991A-23752
                                       US-09-252-991A-23752
                                                                                                                                                                                                                                                                                                                        ; Sequence 23752, Applic
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. 1
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PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3832
LENGTH: 220
                                                                                        NUMBER OF SEQ ID NOS:
SEQ ID NO 23752
LENGTH: 725
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Matches 7; Conserv
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                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                 LENGTH: 725
TYPE: PRT
ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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Pred. No. 4.4e+02;
 Score 35;
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   BB
 2;
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Length 725;
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Query Match

60.3%;

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COUNTRY: U.S.A.

ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/554,612C
FILING DATE: No. 5747660ember 6, 1995
CLASSIFICATION: $36
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION UNMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELEPHONE: (415) 322-5070
TELEPHONE: (415) 322-5070
TELEPAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 819 smino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
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US-09-270-767-60600
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US-08-554-612C-1
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               Sequence 60600, Application US/09270767

Sequence 60600, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 60600
LENGTH: 67
TYPE: PRT
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Fatent No. 5747660
Fatent No. 5747660
GENERAL INFORMATION:
APPLICANT: O'CILICKY, David
TITLE OF INVENTION: PROSTAGLANDIN F2' RECEPTOR REGULATORY
TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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1e8 6; Conservation
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CITY: Menlo Park
STATE: California
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1; Mismatches 4
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US-09-270-767-60600
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Query Match 58.6%; Score 34; DB 2; Length 67; Best Local Similarity 87.5%; Pred. No. 81; Mismatches 0; Indels 0; Gap Matches 7; Conservative 1; Mismatches 0; Indels 0; Gap Qy 1 RKMLKSTR 8
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Search completed: February 4, 2006, 03:43:33 Job time : 31.6667 secs

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Minimum
Maximum
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No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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protein search, using sw
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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16, Appli
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22, Appli
22, Appli
22, Appl
221, Appl
2364, Appl
2405, Appl
279, A
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AL RESULT 1 US-10-790-768A-1 Sequence 1, Application US/10790768A ; Publication No. US20040209797A1 ; GENERAL INFORMATION:	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	,
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1 pplicat o. US20 MATION:	600.33	
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ALIGNMENTS 90768A	US-10-437-963-151528 US-10-733-670-4 US-10-737-963-151528 US-10-427-963-138917 US-10-425-115-261163 US-10-424-599-276649 US-11-97-710-3645 US-10-767-701-3645 US-10-762-115-316007 US-10-425-115-316007 US-10-425-115-319023 US-10-425-115-39023 US-10-425-115-39023 US-10-427-963-108557 US-10-427-963-145925 US-10-427-963-141969	חסתכנו בישם בני חיי
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FILE REFERENCE: 002877.00028
CURRENT APPLICATION NUMBER: US/10/790,768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOPTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
; FEATURE:
; OTHER INFORMATION: protein transduction domain
US-10-790-768A-2
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                                                 APPLICANT: Karas, Michael
TITLE OF INVENTION: Acids
FILE REFERENCE: 002877.00028
CURRENT APPLICATION NUMBER: US/10/790,768A
CURRENT APPLICATION NUMBER: US/10/790,768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOPTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10790768A Publication No. US20040209797A1 GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: Intracellular Delivery
TITLE OF INVENTION: Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: protein transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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Sequence 16, Application US/10790768A

Publication No. US20040209797A1

GENERAL INFORMATION:
APPLICANT: Karas, Michael

TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and
TITLE OF INVENTION: Acids
FILE REFERENCE: 002877.00028

CURRENT APPLICATION NUMBER: US/10/790,768A

CURRENT FILING DATE: 2004-03-03

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.1

SEQ ID NO 16

LENGTH: 15

TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: protein transduction domain FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: Biotin
US-10-790-768A-14
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US-10-790-768A-14
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                                                                                             ; NAME/KEY: MISC_FEATURE
; LOCATION: (1): (1)
; OTHER INFORMATION: Biotin
US-10-790-768A-16
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US-10-790-768A-16
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CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/10790768A Publication No. US20040209797A1 GENERAL INFORMATION:
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Best Local Similarity
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                        Query Match 100.0%; Score 58; DB 4; Length 15; Best Local Similarity 100.0%; Pred. No. 0.0034; Matches 12; Conservative 0; Mismatches 0; Indels
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                               FEATURE: OTHER INFORMATION: protein transduction domain
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Pred. No. 0.0034;
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Pred. No. 0.0034;
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RESULT 7
US-10-790-768A-20
; Sequence 20, Application US/10790768A
; Publication No. US20040209797A1
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GENERAL INFORMATION:

APPLICANT: KARAS, Michael

ITITLE OF INVENTION: Intracellular Delivery of

ITITLE OF INVENTION: Acids

FILE REFERENCE: 002877.00028

CURRENT APPLICATION NUMBER: US/10/790,768A

CURRENT FILING DATE: 2004-03-03

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.1

SEQ ID NO 19
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Best Local Similarity
Watches 12; Conserve
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
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Publication No. US20040209797A1
GENERAL INFORMATION:
APPLICANT: Karas, Michael
                                                                 Query Match 100.0%; Score 58; DB 4; Best Local Similarity 100.0%; Pred. No. 0.0048; Matches 12; Conservative 0; Mismatches 0
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NAME/KEY: MISC_FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: Biotin
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Conservative
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Pred. No.
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APPLICANT: KAYA8, Michael
APPLICANT: KAYA8, Michael
TITLE OF INVENTION: Intracellular Delivery of
TITLE OF INVENTION: Acids
FILE REFERENCE: 002877.00028
CURRENT APPLICATION NUMBER: US/10/790,768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 21
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US-10-790-768A-5
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                                                                                                                   Sequence 18, Application US/10790768A Publication No. US20040209797A1 GENERAL INFORMATION:
APPLICANT: Karas, Michael
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SEQ ID NO 5
LENGTH: 27
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APPLICANT: Karas, Michael
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CURRENT APPLICATION NUMBER: US/10/790,768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
                                                       TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, TITLE OF INVENTION: Acids FILE REFERENCE: 002877.00028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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OTHER INFORMATION: Biotin
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100.0%; Pred. No. 0.0
tive 0; Mismatches
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: protein transduction domain
FEATURE:
NAME/KBY: MISC FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: Biotin
US-10-790-768A-18
                                                                                                                                                  US-10-790-768A-22
, Sequence 22, Application US/10790768A
; Sequence 22, Application US/10790768A
; Publication No. US20040209797A1
; GENERAL INFORMATION:
, APPLICANT: Karas, Michael
; TITLE OF INVENTION: Acids
; TITLE OF INVENTION: Acids
; TITLE OF INVENTION: Acids
; TITLE REFERENCE: 002877.00028
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Best Local Similarity
Marches 10; Conserva
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Best Local S
Matches 10
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APPLICANT: Karas, Michael
TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and
TITLE OF INVENTION: Acids
FILE REFERENCE: 002877.00028
                            CURRENT APPLICATION NUMBER: US/10/790,768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 25
TYPE: PRT
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CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
LENGTH: 25
TYPE: PRT
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LENGTH: 19
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OTHER INFORMATION: Biotin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: protein transduction domain
ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                  10 MLKSTRRORR
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Conservative
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Pred. No
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0.22;
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US-09-738-626-3964
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US-10-408-765A-2219
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 2219
                                                                                                                                                                                                                                                                                                             Sequence 3964, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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Best Local Similarity 81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088,465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D. APPLICANT: Zhang, Bing
                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
                                                                                                                                                                                                         APPLICANT:
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TYPE: PRT
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OTHER INFORMATION: Biotin
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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Taylor, Steven W.
Glenn, Gary M.
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Pred. No. 21;
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Sequence 8521, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ONTIKAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, VOSHIYUKI
APPLICANT: SAKAKI, VOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 113033
LENGTH: 172
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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
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US-10-156-761-8521
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3964
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
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Matches 9; Conserv
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APPLICANT:
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ORGANISM: Oryza sativa
FEATURE:
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Local Similarity 66.7%;
hes 8; Conservative
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Wu, Wei
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Cao, Yongwei
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Pred. No.
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; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8521
; SEQ ID NO 8521
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8521

Query Match
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 0; Gaps 0;

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Db 359 RRRLRSRRQRR 370

Search completed: February 4, 2006, 03:47:33
Job time: 105 secs
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Result
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Listing first 45 summaries
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 4, 2006, 03:26:33 ; Search time 310.556 Seconds (without alignments) 21.222 Million cell updates/sec
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ABM47044
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ABOF07212
ABM888910
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AAY41728
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Adc94119
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Adf64119
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54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7
413	413	413	413	413	413	413	413	413	413	413	413	413	413	413	413	413	413	413	413	413
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ABU72236	ABU91736	ABU98030	ABU98815	ABU85655	ABO25230	ABR94682	ABR74920	ABO02766	ABO08714	ABU92637	ABU96206	ABR68153	ABU89904	ABU82783	ABU99544	ABR65604	ABR66214	ABU84340	ABU88025	ABU58477
Abu72236 Novel	Abu91736 Novel	Abu98030 Novel	Abu98815 Novel	Abu85655 Human	Abo25230 Novel	Abr94682 Human	Abr74920 Human	Abo02766 Human	Abo08714 Human	Abu92637 Human	Abu96206 Novel	Abr68153 Human	Abu89904 Novel	Abu82783 Human	Abu99544 Human	Abr65604 Human	Abr66214 Human	Abu84340 Human	Abu88025 Novel	Abu58477 Human
hum	hum	hum	hum	PRO	mng	8eC	sec	960	sec	sec	hum	8eC	hum	PRO	gec	960	960	8ec	mud	PRO

ALIGNMENTS

RESULT 1 ADS17630 04-MAR-2003; 03-MAR-2004; protein transduction domain; PTD; PTD-cargo moiety complex; cell immortalisation; cell viability; internalising peptide; 02-DEC-2004 ADS17630; 16-SEP-2004. Synthetic. cell transport. ADS17630 standard; peptide; 15 AA. 04-MAR-2004; 2004WO-US006445 WO2004078933-A2 Key Modified-site Amino acid sequence of a PTD designated Biotin-Lys-InvRP5. 2003US-0451243P. 2004US-00790768. (first entry) Location/Qualifiers /note= "biotin attached"

The specification describes peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. The present sequence

New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell.

domain,

WPI; 2004-653708/63.

Karas M;

(BIOW-) BIOWHITTAKER TECHNOLOGIES

INC

Example 4; SEQ ID NO 14; 60pp; English.

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ARBSULT 2
ANDS17618
JID 177618
AC ADS1
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RESULT 3
ADS17636
ID ADS17636 standard; peptide; 21 AA
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                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a peptide which functions as a protein transduction domain (PTD), and is capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo molety complexes that can reversibly immortalise cells and increase cell viability in culture. The present PTD has a lysine linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell.
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cell immortalisation; cell viability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of protein transduction domain (PTD) peptide
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                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karas M;
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03-MAR-2004;
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15; Conserv
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                                                                                                                                   KGGRKMLKSTRRQRR 15
                                                                                                                                                                                                                                         100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003US-0451243P.
2004US-00790768.
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                                                                                                                                                                                                                                         Score 75; DB b; red. No. 2.7e-05;
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Pred. No.
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hes 0;
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     RESULT 4
ADS17620
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XX PT 02-F
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Best Local S
Matches 15
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03-MAR-2004;
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The specification describes peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. ADS17634-ADS17638 represent PTD peptides used in an experiment to determine if introduction of a nuclear localisation signal affects translocation of a PTD-cargo moiety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell.
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cell immortalisation; cell viability; internalising peptide;
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protein transduction domain; PTD; PTD-cargo moiety complex;
cell immortalisation; cell viability; internalising peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 10; SEQ ID NO 20; 60pp; English.
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                                                                                                                                                                                                                                                                             ADS17620 standard; peptide; 21 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        KGGRKMLKSTRRORR
                                                                                         sequence of protein transduction domain (PTD) peptide
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2004US-00790768
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   peptide;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a peptide which functions as a protein transduction domain (PTD), and is capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo molety complexes that can reversibly immortalise cells and increase cell viability in culture. The present PTD has a lysine linker and a nuclear localisation signal.
                                                                               04-MAR-2003; 2003US-0451243P.
03-MAR-2004; 2004US-00790768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein transduction domain; PTD; PTD-cargo moiety complex; cell immortalisation; cell viability; internalising peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell transport.
                                                                                                                                                              04-MAR-2004; 2004WO-US006445
                                                                                                                                                                                                                   16-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a PTD designated peptide 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-2004
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03-MAR-2004;
                            (BIOW-) BIOWHITTAKER TECHNOLOGIES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGGRKMLKSTRRQRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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2004US-00790768
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               /note=
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                                                                                                                                                                                                                                                                                                                            "biotin attached"
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Pred. No. 3.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21;
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RESULT 6
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Best Local Similarity
                                                                                                                New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell.
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                                                                                                                                                                                                                                       WPI; 2004-653708/63
                                                                                                                                                                                                                                                                                                                                                                                                               04-MAR-2003;
03-MAR-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAR-2004; 2004WO-US006445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein transduction domain; PTD; PTD-cargo moiety complex; cell immortalisation; cell viability; internalising peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004078933-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-653708/63.
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                                                                                                                                                                                                                                                                                                                                                           (BIOW-) BIOWHITTAKER TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intracellular compartment of a cell.
                                                                                                                                                                                                                                                                                                 Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KGGRKMLKSTRRORR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KGGRKMLKSTRRORR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of a PTD designated Biotin-InvRP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               2003US-0451243P.
2004US-00790768.
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Pred. No. 3.8e-05;
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Example 4; SEQ ID NO 16; 60pp; English.

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Best Local S
Matches 15
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Best Local :
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                                                                                                                                                                                                                                                                                      The present sequence represents a peptide which functions as a protein transduction domain (PTD), and is capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. The present PTD has a lysine linker and 2 nuclear localisation signals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated and purified polypeptide with a protein transduction domain useful for delivering small molecules, proteins and nucleic acids to an intracellular compartment of a cell.
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03-MAR-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein transduction domain; PTD; PTD-cargo moiety complex;
cell immortalisation; cell viability; internalising peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of protein transduction domain (PTD) peptide
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                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 5; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-653708/63
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                                                                                                              Similarity
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2004US-00790768.
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Pred. No. 0.00018;
0; Mismatches 0;
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Pred.
21
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(first entry)

Amino acid sequence of a PTD designated peptide

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell.
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03-MAR-2004; 2004US-00790768
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cell immortalisation; cell viability; internalising peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-653708/63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karas M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 10; SEQ ID NO 18; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOW-) BIOWHITTAKER TECHNOLOGIES
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                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                          KGGRK----MLKSTRRORR 15
                                                                                                                                                                            KGGKKKRKVMLKSTRRORR 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of a
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                                                                                                                                                                                                                                                                                                                                                                                   Score 60; DB 8;
Pred. No. 0.0098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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RESULT 10
ADS17637
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XX Prote
XX Cell
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo molety complexes that can reversibly immortalise cells and increase cell viability in culture. ADS17634-ADS17638 represent PTD peptides used in an experiment to determine if introduction of a nuclear localisation signal affects translocation of a PTD-cargo molety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated and purified polypeptide with a protein transduction domain, useful for delivering small molecules, proteins and nucleic acids to an intracellular compartment of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein transduction domain; PTD; PTD-cargo moiety complex; cell immortalisation; cell viability; internalising peptide; cell transport.
                             Key
Modified-site
                                                                                                                   protein transduction domain; PTD; PTD-cargo moiety complex; cell immortalisation; cell viability; internalising peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25
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03-MAR-2004; 2004US-00790768.
                                                                           Synthetic
                                                                                                                                                               Amino acid sequence of a PTD designated peptide 16.
                                                                                                                                                                                                02-DEC-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karas M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-2004; 2004WO-US006445
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                                                                                                                                                                                                                                                          ADS17637 standard; peptide; 25 AA
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                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                         KGGRK----MLKSTRRQRR 15
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                                                                                                                                                                                              (first entry)
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                                             Location/Qualifiers
               /note= "biotin attached"
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73.7%;
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Pred. No. 0.013;
1; Mismatches
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RESULT 11
ADS17617
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XX ADS17
XX DT 02-DE
XX Prote
KW Prote
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XX WO200
XX WO200
XX WO200
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XX WO300
XX WO16-SE
XX WO3-WB
PR 03-WB
XX O3-WB
XX O3-WB
XX WPI;
XX WPI;
XX WPI;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes peptides which function as a protein transduction domain (PTD), and are capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo moiety complexes that can reversibly immortalise cells and increase cell viability in culture. ADS17634-ADS17638 represent PTD peptides used in an experiment to determine if introduction of a publical localisation signal affects translocation of a PTD-cargo moiety
               WPI; 2004-653708/63
                                                                                                 04-MAR-2003;
03-MAR-2004;
                                                                                                                                           04-MAR-2004; 2004WO-US006445
                                                                                                                                                                                                                                                         protein transduction domain; PTD; PTD-cargo moiety complex; cell immortalisation; cell viability; internalising peptide cell transport.
                                                                                                                                                                                                                                                                                                                                               02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 AA;
                                           Karas M;
                                                                                                                                                                        16-SEP-2004.
                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                             ADS17617;
                                                                                                                                                                                                                                                                                                                                                                                                        ADS17617 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAR-2003;
03-MAR-2004;
                                                                                                                                                                                                    WO2004078933-A2
                                                                                                                                                                                                                                                                                                               Amino acid sequence of protein transduction domain (PTD) peptide
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                                                                     BIOWHITTAKER TECHNOLOGIES
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                                                                                                 2003US-0451243P.
2004US-00790768.
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2004US-00790768.
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Pred. No. 0.013;
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a peptide which functions as a protein transduction domain (PTD), and is capable of delivering small molecules, proteins, and nucleic acids to an intracellular compartment of a cell. An amino terminal lysine linker improves the efficiency of the PTD. The PTD can be used in PTD-cargo molety complexes that can reversibly immortalise cells and increase cell viability in culture. The present sequence is a reverse isomer of ADS17641, a previously identified internalising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated and purified polypeptide with a protein transduction useful for delivering small molecules, proteins and nucleic acids intracellular compartment of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; EIISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12
 pustulosis,
P. acnes is
                                     the
                                                  polypeptides. The proteins and
                                                               Sequences AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                         Example 1;
                                                                                                                            Propionibacterium acnes vaccinating against and
                                                                                                                                                                                                           L'maisonneuve
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02-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium
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                                                                                                                                                                                                                                                 (CORI-)
Typeptides. The proteins and their associated DNA sequences are use e treatment, prevention and diagnosis of medical conditions caused acnes. The disorders include SAPHO syndrome (synovitis, acne, stulosis, hypertosis and osteomyelitis), uveitis and endophthalmitiacnes is also involved in infections of bone, joints and the central acnes is also involved in infections of bone,
                                                                                                                                                                                  2001-616774/71.
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                                                                                                                                                                                                                                                  CORIXA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; protein;
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                                                                                         SEQ ID NO 11720; 1069pp;
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ve J, Zhang
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                                                                                                                              polypeptides and nucleic acids useful diagnosing infections, especially use
                                                                                                                                                                                                           Mitcham ,
Jen S,
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c Carter
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                                                                                         English.
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              and endophthalmitis.
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                                                    are used
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ABM47044
ADM 4704
AC ABM47
XX ACDE Propi
XX ACDE W0200
XX ACDE EMM47
XX ACDE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitcham C
Zhang Y,
Barth B,
encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polymucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM47044 standard; protein;
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                                                                                                                                                                                                                                                                                                                                             New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes predicted ORF-encoded polypeptide #11720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes.
                                                                                                                                                                                                                                  The invention relates to an
                                                                                                                                                                                                                                                                                      Example 1;
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                                                                                                                                                                                                                                                                                         SEQ ID NO 11720; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No.
                                                                                                                                                                                                                                  isolated polynucleotide (ACF64435-ACF64733)
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Benson DR,
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Best Local &
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07-APR-2000;
03-AUG-2000;
                                                                                        Novel polynucleotides mutation point of a ge expression profile or
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Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacterium; as organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium
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2000JP-00159162.
2000JP-00280988.
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Senoh A, Ikeda
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                                                                                         des derived from Coryneform bacteria, a gene, measuring expression of a gene or pattern of a gene and identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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da M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                      S, Hayashi M,
Ozaki A;
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    acnes polypeptides,
populations, or

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. are useful for identifying the mutation point of a gene derived from mutant of coryneform bacterium, measuring expression amount and anal

l from a l analysing

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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease,

comprises detecting a with the disease.

Claim 1; SEQ ID

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2219; 180pp;

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correlating

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRE; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                             Identifying a mitochondrial target for drug screening assays and treating diseases associated with altered mitochondrial function comprises detecting a modified polypeptide in a sample and corre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-2002; 2002US-0372843P
17-JUN-2002; 2002US-0389987P
20-SEP-2002; 2002US-0412418P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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(BUCK-) BUCK INST AGE RES.
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DB;
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Pred. No. 10;
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    Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 18 derived by analysis of the total score distribution.
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seq length: 2000000000
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Match
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1: pir1:*
2: pir2:*
3: pir3:*
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75
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50.938 Million cell updates/sec
                      Gapop 10.0 , Gapext 0.5
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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                                                                       hypothetical prote
protamine P1 - Aus
probable potassium
hypothetical prote
hypothetical prote
ABC transporter AT
glycosyl transfera
conserved hypothet
ribosomal protein
spermatid-specific
hypothetical prote
probable transcrip
hypothetical prote
ribonuclease H rnh
core antigen - her
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protein T2E6.2 [im
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glycerol-3-phospha
glpD gene homolog
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36.5	36.5	37	37	37	37	37	37	37	37	37	37	37	37	37	
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S41628	G71445	S20473	T24230	T10219	G72857	T41806	D70855	F89937	FOAD72	HSUR8P	HSUR6P	FOADH5	S39425	S73486	
genome polyprotein	hypothetical prote	fatty-acid synthas	hypothetical prote	protein kinase hom	late expression fa	LEF-9 orf62 - Bomb	probable ilvC prot	hypothetical prote	major core protein	histone H2B.3, spe	histone H2B.2, spe	major core protein	protamine P1 - duc	ribosomal protein	C 10

ALIGNMENTS

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RESULT 2 A40973 A40973 spermatid-specific protein T1 precursor - common cuttlefish spermatid-specific protein T1 precursor - common cuttlefish N;Alternate names: arginine-rich protamine; testis-specific protein T1 C;Species: Sepia officinalis (common cuttlefish) C;Date: 21-Apr-1992 #sequence revision 21-Apr-1992 #text_change 09-Jul-2004 C;Accession: A40973; 514085 R;Wouters-Tyrou, D.; Chartier-Harlin, M.C.; Martin-Ponthieu, A.; Boutillon, C.; Van Dorse J. Biol. Chem. 266, 17388-17395, 1991 A;Title: Cuttlefish spermatid-specific protein T. Molecular characterization of two variants. A40973; MUID:91373359; PMID:1894625 A;Accession: A40973 A;Accession: A40973 A;Accession: A40973 A;Accession: A40973 A;Cross-references: UNIPROT:P80001; UNIPARC:UPI00001323A4	Qy 1 KGGRKMLKSTRRORR 15 : :: : Db 19 KGGRRRRRSRRRRR 33	Query Match 58.7%; Score 44; DB 2; Length 77; Best Local Similarity 53.3%; Pred. No. 2.3; Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;	RESULT 1 840973 8permatid-specific protein T2 precursor - common cuttlefish NyAlternate names: arginine-rich protemine; testis-specific protein T2 C:Species: Sepia officinalis (common cuttlefish) C:Species: Sepia officinalis (common cuttlefish) C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jul-2004 C;Accession: 840973; S14086 R;Mouters-Tyrou, D.; Chartler-Harlin, M.C.; Martin-Ponthieu, A.; Boutillon, C.; Van Dors J. Biol. Chem. 266, 17188-17395, 1991 A;Title: Cuttlefish spermatid-specific protein T. Molecular characterization of two varials, Accession: 840973 A;Molecule type: protein A;Residues: 1-77 <mou> A;Cross-references: UNIFROT:P80002; UNIFARC:UPT00001323AB A;Cross-reference : UNIFROT:P80002; UNIFARC:UPT00001323AB A;Title: Cuttlefish sperm proteamines. 1. Amino acid sequences of two distinct variants. A;Reference number: \$14086 A;Molecule type: protein A;Residues: 2-77 <mard 2-77="" <mard="" a;<="" a;residues:="" td=""></mard></mou>

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A;Title: Cuttlefish sperm protamines. 1. Amino acid sequences of t A;Reference number: $14085; MUID:91153298; PMID:1999185
A;Recession: $14085
A;Rolecule type: protein
A;Residues: 22-78 <AMAR>
A;Cross-references: UNIPARC:UPI00001771P8
A;Cross-references: UNIPARC:UPI00001771P8
C;Superfamily: sperm histone
C;Superfamily: sperm histone
C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis
F;1-21/Domain: signal sequence #status predicted <SIG-
F;22-78/Product: protamine variant Sp1 #status experimental <AMAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Wouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andula, N.; Kouach, M.; Jaquinod, M.; Siochem. J. 309, 529-534, 1995
A;Title: Squid spermiogenesis: molecular characterization of testis-specific pro-protami A;Reference number: S56116; MUID:95351983; PMID:7626016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spermatid-specific protein T1 - longfin squid
C;Species: Loligo pealeii (longfin squid)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S56116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q7M4G6; UNIPARC:UPI00001771FC C;Superfamily: sperm histone
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A;Reference number: Z21576
A;Accession: T36275
                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SCE68.25c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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A; Residues: 1-79 < WOU>
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A; Residues: 1-32 < MUR>
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Best Local
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Experimental source: strain A3(2)
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                                                                                                                                                                                                                Experimental source: strain
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Best Local Similarity
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Local Similarity 53.3%;
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8; Conser
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        KKHRKLLKRTRVQRR
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                                                                                                            57.3%;
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53.3%; Pred. No. 2.3;
tive 4; Mismatches
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Pred. No. 2.3;
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Pred. No. 1.5;
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                                                                                             Mismatches
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          Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, Sa;Title: Massive gene decay in the leprosy A;Reference number: A86909; MUID:21128732;
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R;Retief, J.D.; Winkfein, R.J.; Dixon, G.H.
Eur. J. Biochem. 218, 457-461, 1993
A,Title: Evolution of the monotremes. The sequences of the A;Reference number: S39424; MUID:94094837; PMID:8269934
A,Accession: S39424
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A; Gene: elkl
C; Keywords: ]
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A;Description: Identification of three rat potassium chann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable potassium channel elk chain 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
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C;Superfamily: sperm hi
C;Keywords: DNA binding
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A; Residues: 1-69 < RET>
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R;Retief, J.I
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C;Species: Tachyglossus aculeatus (Australian echidna)
C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #te
hypothetical protein ML242BA [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accesion: A87213 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accesion: Associated as a sequence as a seq
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A;Residues: 1-1017 <ENG>
A;Cross-references: UNIPROT:Q9R1T9;
A;Cross-references: cortex
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A; Accession: T31354
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                                                        N.R.; Wheeler, A.; Hamlin, N.;
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S.; Simmonds, M.;

Skelton,

J.; Squares,

PS

bacillus. PMID:11234002

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C;Accession: AE1979

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AE1979
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Bubmitted to the EMBL Data Library, December

The sequence of S. cerevisiae
                      A;Experimental source: strain C;Genetics; A;Gene: alr1384
                                                                                                   A;Statue: preliminary
A;Molecule type: DNA
A;Residues: 1-361 <KUR>
                                                                                                                                                                                                                                                                                            ABC transporter ATP-binding protein alr1384 [imported] - Nostoc sp. (strain PCC C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001  
#sequence_revision 14-Dec-2001  
#text_change 31-Dec-2004
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C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
C;Accession: S43220; SS0630
R;Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, submitted to the EMBL Data Library, February 1993
                                                             A;Cross-references: UNIPROT:Q8YX34; UNIPARC:UPI00000CE09F; GB:BA000019; PIDN:BAB73341.1
A;Experimental source: strain PCC 7120
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A, Residues: 1-357 <DIE>
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A,Status: preliminary
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Residues: 1-357 <MUL>
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Map position: 5R
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2; Mismatches
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Pred. No. 42;
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    Bacteriol. 183, 5709-5717, 2001
    Bacteriol. 183, 5709-5717, 2001
    Pauthors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A; Talle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
    A; Reference number: A97872; MUID:21429245; PMID:11544234

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A;Molecule type: DNA
A;Residues: 1-441-KUR-
A;Cross-references: UNIPROT:Q97QX1;
A;Experimental source: strain TIGR4
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A; Residues: 1-441 < KUR>
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                                                                                                                                                                                              A;Cross-references: UNIPROT:Q8CWR6; UNIPARC:UPI00000E493B; GB:AE007317; PIDN:AAK99786.1;
                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                            A; Accession: F97994
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A;Accession: D95124
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                                      1 KGGRKMLKSTRRQ 13
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KGSRRMLKASKTQ 428
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Pred. No. 43;
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tz, E.J.; Lu, J.; Matsushima, P.; McAhren,
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Lewis, M.R.;
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Radune, D.; Holtzapple,
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protein

L34 [imported]

Listeria monocytogenes (strain EGD-e)

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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, A;Authors: Kreft, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. ok, C.; Schlueter, T.; Simoes of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
C;Accession: AG1431
C;Accession: AG1431
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend,
                                                                                                                                                                          RESULT 14
S56117
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A; Authors: Kreft, T.; Schlueter, T.; Sismoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AE1805
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A; Experimental source: strain EGD-e
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             spermatid-specific protein T2 precursor - longfin squid
N;Alternate names: sperm protamin SP
C;Species: Loligo pealeii (longfin squid)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S56117
R;Wouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andula, N.; Kouach, M.; Jaquinod,
Biochem. J. 309, 529-534, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: rpmr
C;Superfamily: Escherichia coli ribosomal protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ribosomal protein L34 (imported) - Listeria innocua (strain Clip11262)
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A;Title:
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A; Residues: 1-44 <GLA>
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;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
;Accession: AE1805
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;Experimental source: strain Clip11262
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spermiogenesis: molecular characterization of testis-specific pro-protami
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Dussurget, O.; Entian, K.D.; Fsihi, H.
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Dussurget, O.; Entian,
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Voss, H.; Wehland
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Fsihi, H.
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A;Reference number: S56116; MUID:95351983; PMID:7626016
A;Accession: S56117
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-118 <WOU>
A;Cross-references: UNIPROT:Q7M4A3; UNIPARC:UPI000017BDD7
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                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T05A6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24499
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A; Residues: 1-258 <WIL>
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L Nature 424.1037-1042(2003).

C -|- SIMILARITY: Contains 1 PDZ (DHR) domain.

EMBL, BX56969; CAE07123.1; -; Genomic DNA.

R GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0004295; F:trypsin activity; IEA.

R GO; GO:0004295; F:trypsin activity; IEA.

R GO; GO:0004295; F:trypsin activity; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001478; DDZ.
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InterPro; IPR001254; Peptidase_S1_S6.
Pfam; PF000595; PD2; 1.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00834; PROTEASESIC.
SMART; SM00228; PD2; 1.
SMART; SM00220; Tryp SPC; 1.
PROSITE; PS50106; PDZ; 1.
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Q4NDY7;
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Hammon N., Israni S., Pitluck S., Richardson P.,
"Sequencing of the draft genome assembly of Arthrobacter
submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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PubMed=15286373; DOI=10.1126/science.1100330;

Brueggemann H., Henne A., Hoster F., Liesegang H.,

Strittmatter A., Hujer S., Duerre P., Gottschalk G.

"The complete genome sequence of Propionibacterium

"The mann skin.";

Science 305:671-673(2004).

EMBL, AE017283; AAT82076.1; -; Genomic_DNA.
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10-NAY-2005 (Rel. 47, Last annotation update)
Spermatid-specific protein T2 [Contains: Sperm protami
Segia officinalis (Common cuttlefish).
Eukaryota, Metazoa; Mollusca; Cephalopoda; Coleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEPOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome; Hypothetical SEQUENCE 33 AA; 4073 MW; 42
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Bacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterineae; Propionibacteriaceae; Propionibacterium
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                                                                                                                                                                                                                                                                                                                                Boutillon C., van Dorsselaer A., Sautiere P.;
"Cuttlefish spermatid-specific protein T. Molecular characterization
of two variants Tl and T2, putative precursors of sperm protamine
variants Spl and Sp2.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1747;
                                                                                                                                                                                    PROTEIN SEQUENCE OF 22-77.
MEDLINE=91133298; PubMed=1999185;
Marcin-Ponthieu A., Wouters-Tyrou D.,
Schindler P., van Dorsselaer A.;
                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE.
MEDLINE=91373359;
Wouters-Tyrou D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6610;
                                                                                                                                           variants.";
                                                                                                                                                                 "Cuttlefish sperm
                                                                                                                                                                                                                                                                                                          Biol.
                        FUNCTION: Cuttlefish spermiogenesis is characterized by a conuclear protein transition: histones -- spermatid-specific proteins (T1/T2) -- protamines (S91/SP2). The protamines capperm DNA into a highly condensed, stable and inactive compounds.
sperm DNA into a highlesubcellular LOCATION:
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                                                                                                                     Biochem. 195:611-619(1991).
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                                                                                                                                                                 protamines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1894625;
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       Nuclear.
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Pred. No. 2.
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                             protamines compact inactive complex.
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TISSUE SPECIFICITY:

Testis

DEVELOPMENTAL STAGE: Spermlogences.

PTM: Phosphorylation occurs at different degrees.

PTM: Phosphorylated form may be predominant in T2. (

rhosphorylated in elongated spermatids, but dephorylated in elongated spermatids)

n T2. SP2 appears dephosphorylated

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SP2 The

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RESULT
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Best Local
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 20, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
spermatid-specific protein T1 [Contains: Sperm protami sepia officinalis (Common cuttlefish).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEPOF
PRT1_S
                                                                                                                                                                                                                    PROTEIN SEQUENCE.

MEDLINE-91373359; PubMed-1894625;

Wouters-Tyrou D., Chartier-Harlin M.-C., Martin
Boutillon C., van Dorsselaer A., Sautiere P.;

"Cuttlefish spermatid-specific protein T. Molec
of two variants T1 and T2, putative precursors

variants Sp1 and Sp2.";

J. Biol. Chem. 266:17388-17395(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPBIAS
VARIANT
                                                                                                                                                           Martin-Ponthieu A., Wouters-Tyrou D., Schindler P., van Dorsselaer A.;
                                                                                                                                                                                   PROTEIN SEQUENCE (MEDLINE-91153298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGION
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                                                                                                                                                "Cuttlefish sperm
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               removed
FUNCTION: Cuttlefish spermiogenesis is characterized by a dou nuclear protein transition: histones -> spermatid-specific proteins (TI/T2) -> protemines (SPI/SP2). The protemines comp sperm DNA into a highly condensed, stable and inactive comple SUBCELLULAR LOCATION: Nuclear.

TISSUE SPECIFICITY: Testis.

DEVELOPMENTAL STAGE: Spermiogenesis.

PTW: Phosphorylated form may be predominant in TI. SP1 appears phosphorylated in elongated spermatids, but dephosphorylated in elongated spermatids, but dephosphorylated
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sin sequencing; DNA condensation; DNA-binding;
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ly; Nuclear protein;
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; PubMed=1999185;
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Pred. No. 5.
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Missing (in T2B).
0F2C1B215292E0D7 CRC64
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e P.;
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                                                                                                                                                                                                                                                            Molecular characterization
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Q7M4G6;
01-MAR-2004 (
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REGION
COMPBIAS
VARIANT
                                                                     Spermatid-specific protein T1.
Loligo pealeii (Longfin squid).
Eukaryota; Metazoa; Mollusca; C
                                                                                                                         01-MAR-2004 (TrEMBLrel. 26, Creat
01-MAR-2004 (TrEMBLrel. 26, Last
01-MAR-2004 (TrEMBLrel. 26, Last
                              NCBI_TaxID=6621;
                                                    Eukaryota; Metazoa;
Decapodiformes; Lol
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Q86C60;
LOLOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=15461424; DOI=10.1007/800239-004-2589-8;
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Decapodiformes; Lol
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Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lewis J.D., de Jong M.E., Bagha S.M., Tang A., Gi
"All roads lead to arginine: the squid protamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Swiss-Prot entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EX European Bioinformatics Institute. There are no rest
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AY269798; AAP32169.1; -;
NCE 78 AA; 10651 MW; F
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8; Conserv
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                                                                                                                                                                                                      PRELIMINARY;
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                                                      Loliginidae;
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                                                      Loligo.
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4; Mismatches
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Pred. No.
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                                                                     Cephalopoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                FD446437AF1B3278 CRC64;
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PROTEIN SEQUENCE

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RESULT 10
QRCODE MOUSE PRELIMINARY;
ID QRCODE,
AC QRCODE,
DT 01-MAR-2003 (TrEMBLrel. 23,
DT 01-MAR-2004 (TrEMBLrel. 26,
DT 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT OR SHAPE OF SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOR RETARE
       SALE E E E B SOO
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Biochem. J. 309 ( Pt 2):529-534(1995)
PIR; S56116; S56116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Squid spermiogenesis: molecular characterization of pro-protamines.";
                                                                            OBCOD6;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030466M24 product:similar to DJ223E3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wouters-Tyrou D., Martin-Ponthieu A., Ledoux-Andul Jaquinod M., Subirana J.A., Sautiere P.; "Squid spermiogenesis: molecular characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein p0571D04.112.
Name=P0571D04.112;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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                               Eukaryota;
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SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2001) to the EMBL; AP004315; BAC65921.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Oryza sativa nipponbare(GA3) genomic clone:P0571004.";
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                                                    musculus (Mouse)
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TENCE 79
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8; Conserv
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       ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cal protein.
173 AA; 18
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Subirana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10788 MW;
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       Euarchontoglires;
                                  Chordata;
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Pred. No. 5.8;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44;
Pred. No.
Craniata; veruca
ralires; Glires;
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                                                                                                                                                                                                                                                                                           409
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14;
          Vertebrata; Eute
lires; Rodentia;
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                               Euteleostomi,
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          Sciurognathi;
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

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the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome
60,770 full-length cDNAs.";
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GO, GO:0005615; C.arrea.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030424122 product:similar to DV223E3.1
enriched library clone:6030424122 product:similar to DV223E3.1
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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RA Miraya R., Hayashizaka Y., Sasaki D., Shibata K., Shinagawa A.,
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CSTBL/GJ; TISSUE=Testis;

STRAIN=CSTBL/GJ; TISSUE=Testis;

MEDLINB=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

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Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

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"RIKEN integrated sequence analysis (RISA) system=384-format

sequencing pipeline with 384 multicapillary sequencer.";
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MEDLINE-20499374; PubMed-11042159; DOI=10.1101/gr.145100;
MEDLINE-20499374; PubMed-11042159; DOI=10.1101/gr.145100;
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Mearaki Y., Muramateu N., Hayashizaki Y., Konno H., Okazaki Y., Muramateu N., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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"Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
NUCLEOTIDE SEQUI
STRAIN=C57BL/6;
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TISSUE=Eye;

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RESULT 12
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RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
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Best Local
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MGI; MGI:2444800; Prss35.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR001254; Peptidase S1 S6.
InterPro; IPR001314; Peptidase S1Ā.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITG; PS00134; TRYPSIN HIS; UNKNOWN_1.
Hydrolase; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 6 days neonate head cDNA, RIXEN full-length enriched
library, clone:5430417J04 product:similar to DJ223E3.1 (PUTATIVE
SECRETED PROTEIN ZSIG13), full insert sequence.
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                                                                                                  Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                          NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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      NUCLEOTIDE SEQUENCE
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BC075675; AAH75675.1; -; mRNA.
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Ich M., Ishii Y., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kadachi J., Fukuda S., RA Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanghaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Kugami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
MIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
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MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs t
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
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the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
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60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Head;
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                                               Ensembl; ENSMUSG00000033491; Mus muscumGI; MGI:2444800; Prss35.
GO; GO:0005615; C:extracellular space;
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STRAIN=C57BL/6J; TISSUE=Head;
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                                                                                                                                        ENSMUSG00000033491; Mus musculus.
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Peptidase_S1_S6
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Harada A.,
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RESULT 13

QTPZL1 ANG
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(07 STRCO

Q9WX07 STRCO |

Q9WX07;

Q9WX07;

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QTPZL1;
Q1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Q1-MAR-2004 (Fragment).
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                                     01-NOV-1999
01-JUN-2003
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.
Hydrolase; Protease; Serine protease.
      Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; GO:0005524; F:ATP binding; IEA.
InterPro; IPR003959; AAA ATPase centr.
InterPro; IPR000048; IQ_region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Anopheles gambiae Sequence Committee, "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles gambiae Sequence Committee; mitted (APR-2004) to the EMBL/GenBank/DBD databases CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry of EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.; AAAB01008986; EAA00378.2; -;
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PF00612; IQ; 1.
IE; PS50096; IQ; 1.
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(TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last seq
(TrEMBLrel. 24, Last ann
protein SCO3327.
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46.7%;
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5B67E1DCF48C2784 CRC64;
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Best Local :
                                                                            Linke B., Tauch A.;
Submitted (DEC-2004) to the
EMBL; CR931997; CAI38085.1;
                                                                                                                                                                                                                                                                                                                                 ORFNames=jk1904;
Corynebacterium jeikeium (strain K411).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinoae: Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21996410; PubMed=12000953; DOI=10.1038/417141a; Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Ruther S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Marren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                           "Complete Genome Sequence and Analysis of the Multi
Nosocomial Pathogen Corynebacterium jeikeium K411,
Bacterium of the Human Skin Flora,";
J. Bacteriol. 187:4671-4682(2005).
                                                                                                                                                                                                                              PubMed=15968079; DOI=10.1128/JB.187.13.4671-4682.2005; Tauch A., Kaiser O., Hain T., Goesman A., Weisshaar B., Isachoff N., Brune I., Chakraborty Albersmeier A., Bekel T., Bischoff N., Brune I., Chakraborty Kalinowski J., Meyer F., Rupp O., Schneiker S., Viehoever P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 417:141-147(2002)
EMBL; AL939116; CAB45361.1;
PIR; T36275; T36275
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hopwood
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l Similarity
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2) / M145;
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           57.3%;
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31,
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                                                                            EMBL/GenBank/DDBJ
-; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation updat
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              Score 43;
Pred. No.
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           Pred.
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Pred. No. 3.
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Mismatches
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ikeium K411, a Lipid-Requiring
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                          DB
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                                                                                            databases
                                                    CRC64;
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                        Length 33;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                       40.5
         Query
Match
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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75
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32.351 Million cell updates/sec
                                      572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGGRKMLKSTRRQRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
     GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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 US-09-605-703B-2766
US-09-107-532A-3699
US-09-543-681A-4404
US-09-252-991A-25958
US-09-999-833A-296
US-10-020-445A-296
US-09-252-991A-27153
US-09-252-991A-27153
US-09-538-092-254
US-09-538-092-254
US-09-538-101C-3904
US-09-538-101C-3968
US-09-134-101C-3668
US-09-134-101C-3668
US-09-132-210-948
US-09-732-210-948
US-09-732-210-948
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Sequence 2766, Ap Sequence 4004, Ap Sequence 296, App Sequence 296, App Sequence 296, App Sequence 27153, App Sequence 27153, App Sequence 3763, App Sequence 3763, App Sequence 4820, App Sequence 4820, App Sequence 16606, A Sequence 110732, App Sequence 10732, App Sequence 10732, App Sequence 10732, App Sequence 29687, App Sequence 29687, App Sequence 10732, App Sequence 10732, App Sequence 25830, App Sequence 25830, App Sequence 25830, App Sequence 298162, App Sequence 933, App Sequence 933, App Sequence 933, App Sequence 948, 
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3
738	704	639	575	351	345	313	309	299	299	248	237	187	174	174	174	173	158
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US-08-864-038A-3	US-09-252-991A-17523	US-09-252-991A-28453	US-09-252-991A-25723	US-09-107-433-4511	US-09-134-000C-5685	US-09-252-991A-28257	US-09-252-991A-27914	US-09-631-548-2	US-08-879-098-2	US-09-252-991A-32920	US-09-248-796A-20114	US-09-949-016-8739	US-09-949-016-6589	US-09-234-613-27	US-08-933-750C-27	US-09-107-532A-4569	US-09-949-016-7013
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
3, Appli	17523, A	28453, A	25723, A	4511, Ap	5685, Ap	28257, A	27914, A	Appli	2, Appli	32920, A	20114, A	8739, Ap	6589, Ap	27, Appl	27, Appl	•	7013, Ap

ALIGNMENTS

Query Match Query Match S7.3%; Score 43; DB 2; Length 33; Best Local Similarity 66.7%; Pred. No. 2.3; Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0; Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0; Qy 1 KGGRKMLKSTRRORR 15	RESULT 1 US-09-605-703B-2766 (Sequence 2766, Application US/09605703B Patent No. 69629B9 GENERAL INFORMATION: APPLICANT: Fompejus, Markus APPLICANT: Kroger, Burkhard APPLICANT: Schroder, Hartwig APPLICANT: Schroder, Hartwig APPLICANT: Haberhauer, Gregor TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING TITLE OF INVENTION UNMBER: US/09/605,703B CURRENT APPLICATION NUMBER: US/09/605,703B CURRENT FILING DATE: 1999-07-08 PRIOR APPLICATION NUMBER: 60/142,764 PRIOR FILING DATE: 1999-09-03 NUMBER OF SEQ ID NOS: 2934 SEQ ID NO 2766 CRGANISM: Corynebacterium glutamicum US-09-605-703B-2766
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US-09-543-681A-4404
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                                                                                                                                       SEQ ID NO 4404
LENGTH: 248
TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                     APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                    Sequence 4404, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                     TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
                                                                                                                             -09-543-681A-4404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...174
SEQUENCE DESCRIPTION: SEQ ID NO: 3699:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                            8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 174 amino acids TYPE: amino acid
                              GGRKMLKSTRROR 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                             56.0%;
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                                                             Score 42; DB
Pred. No. 23;
3; Mismatches
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                                                                             DB 2;
23;
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Patent No. 6551795

PAURITION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27
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NUMBER OF SEQ ID NOS:
SEQ ID NO 25958
LENGTH: 537
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                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630PIC65 CURRENT APPLICATION NUMBER: US/09/999,833A CURRENT FILING DATE: 2001-10-24 PRIOR APPLICATION NUMBER: 09/918585 PRIOR APPLICATION NUMBER: 09/918585 PRIOR PILING DATE: 2001-07-30 PRIOR PILING DATE: 2001-07-30 PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P.
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7; Conserva
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Shelton, David L.
Stewart, Timothy A.
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Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                             Gurney, Austin L.
Hillan, Kenneth J
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Pred. No.
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PRIOR PRIOR

DR APPLICATION NUMBER: 60/064249
DR FILING DATE: 1997-11-03
DR APPLICATION NUMBER: 60/065311
DR FILING DATE: 1997-11-21
DR APPLICATION NUMBER: 60/077632
DR FILING DATE: 1999-03-10
DR APPLICATION NUMBER: 60/077641
DR APPLICATION NUMBER: 60/0776904
DR APPLICATION NUMBER: 60/0776904
DR APPLICATION NUMBER: 60/078936
DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/078936
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079294
DR APPLICATION NUMBER: 60/079294
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079294
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079266
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079266
DR APPLICATION NUMBER: 60/079266
DR APPLICATION NUMBER: 60/07926
DR APPLICATION NUMBER: 60/08013
DR APPLICATION NUMBER: 60/08016
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RESULT 6
US-10-020-445A-296
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-31
PRIOR APPLICATION NUMBER: 60/065361
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/067450
PRIOR APPLICATION NUMBER: 60/077450
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Best Local S
Matches
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APPLICANT:
APPLICANT:
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C74
CURRENT APPLICATION NUMBER: US/10/020,445A
CURRENT FILING DATE: 2001-10-24
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DR FILING DATE: 1998-05-15
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085689
DR APPLICATION NUMBER: 60/085689
DR APPLICATION NUMBER: 60/085579
DR APPLICATION NUMBER: 60/085579
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/08580
DR APPLICATION NUMBER: 60/08580
DR APPLICATION NUMBER: 60/08573
DR APPLICATION NUMBER: 60/08573
DR APPLICATION NUMBER: 60/085704
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DR APPLICATION NUMBER: 60/085697
DR APPLICATION NUMBER: 60/085697
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6962797
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Baker Kevin P.
Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fong,
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Gerritsen, Mary E.
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Jami, Nicholas F.
Jami, Nicholas F.
Jami, Nargaret Ann
David L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Napoleon
f, Ellen
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OR APPLICATION NUMBER: 60/080194
OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/080327
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080328
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080333
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080334
OR FILING DATE: 1998-04-01
OR FILING DATE: 1998-04-08
OR FILING DATE: 1998-04-08
OR FILING DATE: 1998-04-08
OR FILING DATE: 1998-04-08
OR APPLICATION NUMBER: 60/081071
OR FILING DATE: 1998-04-08
OR APPLICATION NUMBER: 60/081195
OR PILING DATE: 1998-04-08 DR FILING DATE: 1998-03-27

DR APPLICATION NUMBER: 60/079728

DR FILING DATE: 1998-03-27

DR APPLICATION NUMBER: 60/079786

DR FILING DATE: 1998-03-27

DR APPLICATION NUMBER: 60/079920

DR FILING DATE: 1998-03-30

DR APPLICATION NUMBER: 60/079923

DR APPLICATION NUMBER: 60/079923

DR APPLICATION NUMBER: 60/080105

DR APPLICATION NUMBER: 60/080107

DR APPLICATION NUMBER: 60/080107

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DR APPLICATION NUMBER: 60/080105

DR APPLICATION NUMBER: 60/080105 R FILING DATE: 1998-03 R APPLICATION NUMBER: (R FILING DATE: 1998-03 R APPLICATION NUMBER: (APPLICATION NUMBER: 60/081955 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081819 APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/079689 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079663 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: 60/078936 FILING DATE: 1998-03-20 FILING DATE: 1998-03-13 APPLICATION NUMBER: 60/078886 FILING DATE: 1998-0: APPLICATION NUMBER: FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/077791 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 1998-03-27 1998-03-20 1998-03-10 1998-03-26 1998-03-1998-04-15 1998-03-25 1998-03-20 1998-03-1998-03-11 60/079664 60/079656 60/078939 60 60/078004 60/077649 60/077632 60/079294 60/081952 /078910

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PRIOR PELLICATION NUMBER: 60/08188
PRIOR PILING DATE: 1998-04-21
PRIOR PILING DATE: 1998-04-21
PRIOR PILING DATE: 1998-04-21
PRIOR PILING DATE: 1998-04-22
PRIOR PILING DATE: 1998-04-23
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-30
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PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-05-05
PRIOR PILING DATE: 1998-05-0
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; TYPE: PRT ; ORGANISM: Pseudomonas US-09-252-991A-23752
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SEQ ID NO 22842
LENGTH: 660
TYPE PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22842
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PRIOR APPLICATION NUMBER: 60/08550
PRIOR APPLICATION NUMBER: 60/085573
PRIOR APPLICATION NUMBER: 60/08573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Best Local S
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23752
LENGTH: 725
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22842, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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Matches
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  Query Match
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

PILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR PPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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9; Conserv
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Pred.
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US-09-538-092-254

US-09-538-092-254

; Sequence 254, Application US/09538092

; Patent No. 6753314
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US-09-134-001C-3904
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                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT FILING LATE: 1998-08-13
PRIOR APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1999-08-14
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3904
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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SQ ID NO 27153
LENGTH: 204
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3904,
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Best Local Similarity
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Best Local
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus epidermidis
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                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                              REGIKLVKPIREQ 15
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Pred. No. 32;
3; Mismatches
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US-09-252-991A-32828
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                                                                                                                                                            US-09-583-110-3763
                                                                                                                                                                               RESULT 13
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PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 254
LENGTH: 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US O
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEO ID NOS: 33142
SEQ ID NO 32828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32828, Application US/09252991A Patent No. 6551795
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                                                                                                                    Sequence 3763, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YER127W
CURRENT APPLICATION NUMBER: US/09/583,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 408
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Pred. No.
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Pred. No. 76;
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67;
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US-09-107-433-4820
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                                                                                                                                                                         APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY AGENT INFORMATION:
NAME: ARINIALION, PAMELA DENEKE
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 4820:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4820, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SEQ ID NO 3763
LENGTH: 441
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PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
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APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
FRIOR APPLICATION DATA:
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NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...442
SEQUENCE DESCRIPTION: SEQ ID NO: 4820:
                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                 FEATURE:
                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5206 CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: <Unknown>
                                                                                ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: <Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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BER: US 09/107,433
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Pred. No. 82;
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Best Local S
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REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 4454:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE SEG ID NO: 4504:
SEQUENCE CHARACTERISTICS:
                                                                     Matches
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Patent No. 6800744
GENERAL INFORMATION:
                                                                                       Best
                                                                                                    Query Match
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COMPUTER: CUNKNOWN'S
OPERATING SYSTEM: CUNKNOWN'S
OPERATING SYSTEM: CUNKNOWN'S
OPERATING SYSTEM: CUNKNOWN'S
SOFTWARE: CUNKNOWN'S
CURRENT APPLICATION NUMBER: US/09/107,433
PILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/ 085131
PILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniallo, Pamela Deneke
                                                                                     Local
                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...85
SEQUENCE DESCRIPTION: SEQ ID NO: 4.
                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                          FEATURE:
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5206
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7; Conserv
                     1 KGGRKMLKSTRRQ 13
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                                                                    Similarity 53.
KGGNOMVVKTRKO
                                                                                                                                                                                                                        ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                          NAME/KEY:
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                                                                                  52.0%;
53.8%;
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                                                                                    Score 39;
Pred. No.
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Pred. No. 82;
4; Mismatches
                                                                     Mismatches
                                                                                                                                                          4454:
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82;
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Search completed: February 4, 2006, 03:43:34

Job time : 39.3333 secs

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No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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Match
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1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/US10A PUBCOMB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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    4, 2006, 03:42:34; Search time 130 Seconds (without alignments)
48.211 Million cell updates/sec
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US-10-790-768A-14
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Sequence 276649,
Sequence 1772, Ap
Sequence 25169,
Sequence 347520,
Sequence 89, Appl
Sequence 296, App
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Sequence 14, Appli
Sequence 4, Appli
Sequence 19, Appl
Sequence 20, Appl
Sequence 5, Appli
Sequence 16, Appli
Sequence 11, Appli
Sequence 21, Appli
Sequence 22, Appli
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RESULT 1 US-10-790-768A-2

ALIGNMENTS

FILE REPERENCE: 002877.00028 CURRENT APPLICATION NUMBER: US/10/790,768A CURRENT FILING DATE: 2004-03-03 NUMBER OF SEQ ID NOS: 25 SOFTWARE: PatentIn version 3.1 SEQ ID NO 2 LENGTH: 15 TYPE: PAT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: protein transduction domain INS-10-790-7508-7 밁 ş US-10-790-768A-14 US-10-790-768A-2 Sequence 14, Application US/10790768A Publication No. US20040209797A1 GENERAL INFORMATION: APPLICATION: Arichael TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic TITLE OF INVENTION: Acids FILE REFERENCE: 002877.00028 FILE REFERENCE: 002877.00028 CURRENT APPLICATION NUMBER: US/10/790,768A CURRENT FILING DATE: 2004-03-03 NUMBER OF SEQ ID NOS: 25 SOFTWARE: Patentin version 3.1 SEQ ID NO 14 LENGTH: 15 TYPE: PRT ORGANISM: Artificial Sequence Sequence 2, Application US/10790768A Publication No. US20040209797A1 GENERAL INFORMATION: APPLICANT: Karsas, Michael TITLE OF INVENTION: Acids TITLE OF INVENTION: Acids Query Match Best Local (Matches FEATURE: OTHER INFORMATION: protein transduction domain FEATURE: 1 KGGRKMLKSTRRORR 15 Similarity Conservative 100.0%; Score 75; DB 4; 100.0%; Pred. No. 1.4e-05; <u>.</u> Mismatches of Small Molecules, Proteins, and Nucleic Length 15; 0 Gaps 0

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Query Match
Best Local Similarity
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                                                                                  ; FEATURE;
; OTHER INFORMATION: protein transduction domain; FEATURE;
; NAME/KEY: MISC_FEATURE; LOCATION: (1)...(1); OTHER INFORMATION: Biotin
US-10-790-768A-19
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TITLE OF INVENTION: Acids
FILE REFERENCE: 00287, 00288
CURRENT APPLICATION NUMBER: US/10/790,768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                    TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic TITLE OF INVENTION: Acids
FILE REFERENCE: 002877.00028
CURRENT APPLICATION NUMBER: US/10/790,768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 21
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Best Local
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APPLICANT: Karas, Michael
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ORGANISM: Artificial Sequence
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Similarity 100.0%;
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              100.0%; Score 75; DB 4; Length 21; ilarity 100.0%; Pred. No. 2e-05; Conservative 0; Mismatches 0; Indels
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Pred. No. 1.4e-05;
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; NAME/KEY: MISC_FEATURE
; LOCATION: (1): (1)
; OTHER INFORMATION: Biotin
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                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/10790768A

Publication No. US20040209797A1

GENERAL INFORMATION:

APPLICANT: Karas, Michael

TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic

TITLE OF INVENTION: Acids

FILE REFERENCE: 00287.00028

CURRENT APPLICATION NUMBER: US/10/790,768A

CURRENT FILING DATE: 2004-03-03

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.1

SEQ ID NO 16
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CURRENT APPLICATION NUMBER: US/10/790,768A

CURRENT FILING DATE: 2004-03-03

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.1

SEQ ID NO 20
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APPLICANT: Karas, Michael
TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and
TITLE OF INVENTION: Acids
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Best Local
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Best Local
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NAME/KEY: MISC FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: Biotin
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Local Similarity 100.0%; les 14; Conservative 0;
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100.0%; Pred. No. 2e-05;
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                                                                    Score 70; DB 4; I; Pred. No. 9.4e-05; 0; Mismatches 0;
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                                                  Sequence 21, Application US/10790768A Fublication NS/20040209797A1 GENERAL INFORMATION:
APPLICANT: Karas, Michael
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APPLICANT: Karas, Michael
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SEQ ID NO 18
LENGTH: 19
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Publication No. US20040209797A1
GENERAL
GENERAL
APPLICANT: Karas, Michael
TITLE OF INVENTION: Intracellular Delivery of Small Molecules,
TITLE OF INVENTION: Acids
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SEQ ID NO 5
LENGTH: 27
TYPE: PRT
ORGANISM: Artificial Sequence
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CURRENT APPLICATION NUMBER: US/10/790,768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
                TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic TITLE OF INVENTION: Acids
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FILE REFERENCE: 002877.00028
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NAME/KEY: MISC_FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: Biotin
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OTHER INFORMATION: protein transduction domain
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14, Conservative
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Pred. No. 0.0056;
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Pred. No. 0.0037;
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; LOCATION: (1)...(1)
; OTHER INFORMATION: Biotin
US-10-790-768A-22
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Sequence 1, Application US/10790768A
Publication No. US20040209797A1
GENERAL INFORMATION:
APPLICANT: Karas, Michael
TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic TITLE OF INVENTION: Acids
FILE REFERENCE: 002877.00028
CURRENT APPLICATION NUMBER: US/10/790,768A
CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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CURRENT FILING DATE: 2004-03-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 25
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Best Local Similarity
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APPLICANT: Karas, Michael
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 25
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ORGANISM: Artificial Sequence
FEATURE:
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NAME/KEY: MISC_FEATURE
LOCATION: (1). (1)
OTHER INFORMATION: Biotin
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ilarity 73.7%;
Conservative
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Pred. No. 0.
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US-10-425-115-335780; Sequence 335780, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
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                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 335780
LENGTH: 71
TYPE: PRT
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APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

Thou, Yihua,
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 117103
LENGTH: 123
TYPE: PRT
ORGANISM: Oryza Bativa
FEATURE:
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
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APPLICANT:
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OTHER INFORMATION: Clone ID: MRT4577_6933C.1.pep
                     ORGANISM: Zea mays
FEATURE:
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Barbazuk, Brad
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69.2%;
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APPLICANT: HAYASHI, MIKIRO
APPLICANT: VOCHIAL, KEIKO
APPLICANT: OCHIAL, KEIKO
APPLICANT: OCHIAL, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
FULE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
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LENGTH: 128
                                                                                                                                                                                                                                                                                                                            Sequence 3964, Application US/09738626 Publication No. US20020197605A1
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LOCATION: (1)..(128)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Cao, Yongwei
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Barbazuk, Brad
Li, Ping
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Pred. No.
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Perfect score:
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DB seq length: 2000000000
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1: /cgn2 6/ptodata/2/pubpas/USOS_NEW_PUB.pep:*

2: /cgn2-6/ptodata/2/pubpas/USOS_NEW_PUB.pep:*

3: /cgn2-6/ptodata/2/pubpas/USO7_NEW_PUB.pep:*

4: /cgn2-6/ptodata/2/pubpas/PCT_NEW_PUB.pep:*

5: /cgn2-6/ptodata/2/pubpas/USO7_NEW_PUB.pep:*

6: /cgn2-6/ptodata/2/pubpas/USO7_NEW_PUB.pep:*

7: /cgn2-6/ptodata/2/pubpas/USO1_NEW_PUB.pep:*

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16.652 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
       KGGRKMLKSTRRQRR 15
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(c) 1993 - 2006 Biocceleration Ltd
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   US-11-037-243-89
US-11-150-054A-21
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US-11-150-054A-30
US-10-821-234-1340
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US-11-165-226-62
US-10-165-226-62
US-10-161-408-50
US-11-024-959-410
US-11-024-959-280
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US-11-024-959-314
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US-11-0467-657-204
US-10-467-657-204
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Sequence 99, Appl
Sequence 10, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 1344, Ap
Sequence 1340, Ap
Sequence 52, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 85, Appl
Sequence 85, App
Sequence 85, App
Sequence 10, App
Sequence 16, App
Sequence 16, App
Sequence 16, App
Sequence 280, App
Sequence 281, App
Sequence 291, App
Sequence 291, App
Sequence 201, App
Sequence 5934, Ap
Sequence 5934, Ap
Sequence 5032, Ap
Sequence 2010, App
Sequence 3632, Ap
Sequence 3632, Ap
Sequence 6390, Ap
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RESULT 2
US-10-689-742-70
US-10-689-742-70
; Sequence 70, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INPORMATION:
   APPLICANT: Jacobs, Kenneth
; APPLICANT: LaVallie, Edward R
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Recie, Lisa A
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
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Merberg, David Treacy, Maurice

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KGGRKMLKSTRRQR : KGGRRRKKSGRGQR	Similarity 9; Conservat	243-89 89, Application 11on No. US2005028 INFORMATION: INFORMAN, GREG ANT: WHYTE, DAVID ANT: CHARVEDEAL, S ANT: CHARVEDEAL, S ANT: MANNING, GER ANT: SUDARSANAN, INT: SUDARSANAN			42.7
KGGRKMLKSTRRQR : KGGRRRKKSGRGQR	y 64.	ion 5028 AVII L, S AGE, NOVI 002/1 NUMBER 0001- 1: 15		211 212 212 213 411 718 871 882 27 27 27 27 27 27 27 27 28 30 30	178 181
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TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM FILE REFERENCE: 00766.000091.10
CURRENT APPLICATION UNMBER: US/10/689,742
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: 09/746,783
PRIOR APPLICATION NUMBER: 09/746,783
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patentin version 3.2
SEQ ID NO 70
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                                       Query Match
Best Local Similarity 50...
7; Conservative
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                                                                                                                                                                                                              SEQ ID NO 13
LENGTH: 54
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                                                                                                                                 OTHER INFORMATION: synthetic peptide -11-150-054A-13
                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/150,054A CURRENT FILING DATE: 2005-06-09 PRIOR APPLICATION NUMBER: 60/578,535 PRIOR FILING DATE: 2004-06-09
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lassner, Michael
APPLICANT: Wilkinson, Jack Q.
TITLE OF INVENTION: Plastid Transit Peptides
FILE REFERENCE: 2119-4284US1
                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (107)...(107) OTHER INFORMATION: Xaa
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                              TYPE: PRT ORGANISM: artificial sequence FEATURE:
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OTHER INFORMATION: Xaa can
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LOCATION: (117)..(118)
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 RRFNRNTRRORR 45
                               RKMLKSTRRORR 15
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RESULT 4

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CURRENT APPLICATION NUMBER: US/11/150,054A
CURRENT FILING DATE: 2005-06-09
PRIOR APPLICATION NUMBER: 60/578,535
PRIOR FILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 57
SOFTWARR: Patentin version 3.3
SEQ ID NO 26
LENGTH: 54
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CURRENT APPLICATION NUMBER: US/11/150,054A
CURRENT FILING DATE: 2005-06-09
FRIOR APPLICATION NUMBER: 60/578,535
PRIOR FILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21
LENGTH: 54
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Best Local Similarity
""" has 7; Conserve
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                                                                                                                                                             RESULT 6
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                                                                                         GENERAL INFORMATION:
                                                                                                          Sequence 1344, Application US/10821234
Publication No. US20050255114A1
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Matches
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APPLICANT: Wilkinson, Jack Q.
TITLE OF INVENTION: Plastid Transit Peptides
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TITLE OF INVENTION: Plastid Transit Peptides
FILE REFERENCE: 2119-4284US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lassner, Michael APPLICANT: Wilkinson, Jack
                                                    APPLICANT: Labat, Ivan APPLICANT: Stache-Crai
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
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Pred. No. 3.3;
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Pred. No. 3
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FILE REPERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOPTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1300
LENGTH: 280
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1344
LENGTH: 154
TYPE: PRT
/ TYPE: PRT
/ ORGANISM: Escherichia coli
US-11-165-211-52
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US-11-165-211-52
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US-10-821-234-1300
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US-10-821-234-1344
                                                                                                                                                                         Sequence 52, Application US/11165211
Publication No. US20050287626A1
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
TITLE OF INVENTION: Process for producing dipeptides
FILE REFERENCE: 4093-14
CURRENT APPLICATION NUMBER: US/11/165,211
CURRENT FILING DATE: 2005-06-24
CURRENT FILING DATE: 2005-06-24
                                                      PRIOR APPLICATION NUMBER: JP2004-189012
PRIOR FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 52
LENGTH: 327
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Publication No. US20050255114A1
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Best Local Similarity 57.1%;
Matches 8; Conservative
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APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 821A
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Pred. No. 26;
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Pred. No. 14;
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APPLICANT: REUBER, T. Lynne
APPLICANT: PINEDA, Omaira
APPLICANT: SHERMAN, Bradley K
ITILE OF INVENTIONS TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
FILE REFERENCE: MBIO058-CIP
CURRENT FLILING DATE: 2003-11-13
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: 10/412,699
PRIOR PILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR PILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 09/505,720
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/53,339
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR PILING DATE: 2000-03-22
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US-11-165-226-62
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US-11-165-226-62
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Sequence 62, Application US/0116527A1

General INFORMATION:

APPLICATION HAKKO KOGYO CO., LTD.

TITLE OF INVENTION: Process for producing dipeptides or dipeptide derivatives

FILE REFERENCE: 4093-13

CURRENT APPLICATION NUMBER: US/11/165,226

CURRENT FILING DATE: 2005-06-24

PRIOR APPLICATION NUMBER: JP2004-189007

PRIOR APPLICATION NUMBER: JP2004-189007

PRIOR FILING DATE: 2004-06-25

NUMBER OF SEQ ID NOS: 131

SOFTWARE: Patentin Ver. 2.1
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT: HEARD, Jacqueline
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TYPE: PRT
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RIECHMANN, Jose Lu
CREELMAN, Robert
RATCLIFFE, Oliver
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REPETTI, Peter
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2000-03-2
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Pred. No. 3
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Pred. No. 3
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US-10-453-372-852
; Sequence 852, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
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SEQ ID NO 10
LENGTH: 342
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 410
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                                                                                                                                                                                                                                                                                                                                    Query Match
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TITLE OF INVENTION: CELL CYCLE GENES AND 1
FILE REFERENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FORSTER, RICHARD L. APPLICANT: CONNETT, MARIE B. APPLICANT: EMERSON, SARAH JANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 441
TYPE: PRT
ORGANISM: Pinus radiata
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OTHER INFORMATION: G2053 polypeptide reference sequence; clade identifier
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                Local Similarity
les 9; Conserv
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Similarity 42.9%;
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EMERSON, SARAH JANE
GRIGOR, MURRAY ROBERT
HIGGINS, COLLEEN M.
LUND, STEVEN TROY
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                                                                                                                                                                                                                                                             KGGRKMLKSTRRORR 15
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Pred. No.
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62;

    See File Wrapper or PALM.

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Query Match
Best Local Similarity
Thes 7; Conserve
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SOFTWARE: Cur
SEQ ID NO 856
LENGTH: 844
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Publication No. US20
GENERAL INFORMATION
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NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 852
                                                     PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/789390 PRIOR FILING DATE: 2001-02-23 PRIOR APPLICATION NUMBER: 60/185967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
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PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-08-25
                                                                                                                                           PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
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                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 2001-03-29
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                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-03-19 PRIOR APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-03-0
                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-05-23
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FILING DATE: 2000-03-01
APPLICATION NUMBER: 09/823187
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APPLICATION NUMBER: 60/195792
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                                      CuraSeqList version 0.1
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b. US20060003323A1
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Pred. No.
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u. No. 1.2e+02;
Mismatches
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                                                                                 See File Wrapper or PALM
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Sequence 50, Application US/10161408

Publication No. US20050287647A9

GENERAL INFORMATION:
APPLICANT: Perez, Carl
APPLICANT: Perez, Carl
APPLICANT: Perez, Carl
APPLICANT: Pabijanski, Steven
APPLICANT: Plant Artificial Chromosomes
FILE REFERENCE: 24601-419
CURRENT FILING DATE: 2002-05-30
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: US 60/294,687
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: US 60/294,687
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50
LENGTH: 356
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
TOTHER INFORMATION: Integrase E1748
                                  FILE REFERENCE: 10001 NP
CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT FILING DATE: 2005-06-28
PRIOR APPLICATION NUMBER: 60/594,405
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
SOFTWARE: Patentin version 3.2
SEQ ID NO 162
LENGTH: 543
TYPE: PAT
ORGANISM: Homo sapiens
US-11-169-041-162
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; ORGANISM: Homo sapiens
US-10-453-372-856
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US-11-169-041-162
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US-10-161-408-50
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                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/11169041

Publication No. US20060019284A1

GENERAL INFORMATION:
APPLICANT: Brisetol-Myers Squibb Company
APPLICANT: Brisetol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSIN
TITLE OF INVENTION: COMPAND OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANC
TITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.3%;
Best Local Similarity 50.0%;
Matches 6; Conservative
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 46.7%;
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267
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  45.3%; Score 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 6; Length 356; Pred. No. 74;
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  DB 7;
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Length 543;
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Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps
Qy 3 GRKMLKSTRRORR 15
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Db 36 GQRLLRQRRROLR 48
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Search completed: February 4, Job time : 11.5556 secs

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